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Title:
Perfect score:
Sequence:
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-MODEL-frame+_p2n.model -DEV=xlh
-O_cgn2_1/USPT0_Spool/SporIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-O=cgn2_1/USPT0_Spool/SporIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-DB-GenEmb1 -OFMT-fastap -SUFFIX-Olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blits -START=1 -END=-1 -MATRIX-olip90 -TRANS-human40.cdi -LIST=1000
-DCCALIGN=200 -THR_SCORE-quality -THR_UNIN-8 -ALIGN=50 -MODE-LOCAL -OUTFMT-pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=BORIN682_@CGN_1_1_2425_@runat_23012003_130141_7873 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPDP=60 -YGAPEXT=60 -DELOP=6 -DELEXX=7
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Maximum
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29: em_vi:*
30: em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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and Miwatani, T

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gi:148531

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J. Biol.
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                       Submitted (07-MAR-2000) Botany, Roosevelt Road, Sec. 4, Talpei, Location/Qualifiers
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Chang, G.N. and Ho, K.C.
Direct Submission
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Chang, G.N. and Ho, K.C.
Heat-labile enterotoxin
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Plasmid P307
Plasmid P307
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l (bases 1 to 777)

Dykes,C.W., Halliday,I.J., Hobden,A.N., Read,M.J.

A comparison of the nucleotide sequence of the A s
labile enterotoxin and cholera toxin

FEMS Microbiol. Lett. 26, 171-174 (1985)

Location/Qualifiers
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/trans1_table=11
/product="heat-labile enterotoxin subunit A precursor"
/product="heat-labile enterotoxin subunit A precursor"
/protein_id="AAL55671.1"
/protein_id="AL55671.1"
/db_xref="GI:18026886"
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/trans1ation="MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRSGGLMPRG
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IYVIATAPNMENVNDVLGVYSGHPYEGEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
REYRDRYYRHLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCN
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/db_xref="taxon:562"
/country="Taiwan"
                   /product="heat-labile enterotoxin subunit
/protein_id="AAA98202.1"
/db_xref="GI:150459"
                                                                                                                                                                                        /specific_host="Escherichia
/db_xref="taxon:2472"
/clone="pAT153."
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                                                                  /codon_start=1
/transl_table=11
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   translation="MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRSGGLMPRG/
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Best Local Similarity:
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Hayes,M.V., Harford,S. and Ross,G.W.
Microbiological process
Patent: EP 0145486-A 5 19-JUN-1985;
GLAXO GROUP LIMITED
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Plasmid ENT P307 (enterotoxigenic E.
M15362
M15362.1 GI:148337
LTp gene; heat-labile toxin.
Plasmid ENT (enterotoxigenic E.coli
p370.
                                                                                                                                                                     Yamamoto, T., Gojobori, T. and Yokota, T. Evolutionary origin of pathogenic determinants Escherichia coli and Vibrio cholerae Ol J. Bacteriol. 169 (3), 1352-1357 (1987)
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1 (bases 1 to 777)

Hayes, M.V., Harford, S. and Ross, G.W.
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A04915
A04915.1 GI:412519
                                                                                                                    Clean copy of sequence [1] kindly (22-APR-1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiological process
Patent: EP 0145486-A 7 19-JUN-1985;
                                                                                                                                                                                                                                      plasmids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRSGGLMPRG
HNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVXTSLSLRSAHLAGQSILSGYSTYY
IYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
REYRDRYYRNLNIAPAEDGYRLAGFPPDHQANREEPWIHHAPQGCGNSSRTITGDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA00403.1"
/db_xref="GI:412520"
/translation="""
                                       /plasmid="Plasmid ENT" 90. .866
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135 c 164 g 222 t 1 others
                           /note="Heat-labile toxin
                                                               /organism="Plasmid ENT"
/db_xref="taxon:2463"
              /codon_start=1
                                                                                                     Location/Qualifiers
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/product="labile toxin
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| . .777
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                                                                                                                               T.Yamamoto
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                                                                                                                                                                                                                                                                            clone
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AUTHORS
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SEQ1-65T079 (1-15) x ENSLTPA (1-866)
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                                                             Unreported.
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Plasmid ENT-R
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Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol
J. Bacteriol. 169 (3), 1352-1357 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid ENTR
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/trans1_table=11
/protein_id="AAA24791.1"
/protein_id="AAA24791.1"
/protein_id="AAA24791.1"
/db_xref="GI:148334"
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HNEYFDRGTOMMINLYHAAGFOTGFVRYDDGYVSTSLSLRSAHLAGOSILSGYSTYR
IYVLATAPMINLYHAMGYSSHPYEDGEVSALGGIPYSQIYGWYRVNPGVIDERLHRN
REYRDRYYRNLNIAPAEDGYRLAGFPDDHQAWREEPWIHHAPQGCGNSSRTITGDTCN
RETONLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIKDEL"
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Hneyepgrgynnunlydharcgggtgryryddcyvstslslrsalhaggsilsgystsyy
Iyviatapmynunutgusghpyragevsalcgiysgylycwyrvprgyddeklmr
Reyrdryyrnuniapaedgyrlagfppdhqawreepwihhapqgcgnssrtitgdtcn
                                                                                    /product="Heat labile
155 c 186 g
                                                                                                                                 /note="Heat labile toxin subunit A signal 176. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Plasmid ENTR"
/db_xref="taxon:2462"
/plasmid="Plasmid ENTR"
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                                                                                                                                                                                                                                                                                                                                                                                             /note="Heat labile toxin subunit A precursor"
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/db_xref="GI:148338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat-labile toxin.
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Query Match:
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COMMENT
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ECOTOXA
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                                                1 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly 15
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Primary structure of heat-labile enterotoxin
Escherichia coli pathogenic for humans
J. Biol. Chem. 259 (8), 5037-5044 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxin;
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                                                                                                                                                                                                               46 bp upstream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECOTOXA
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                                                                                                                                                                                                                               298
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                                                                                     ECOTOXA (1-934)
                                                                                                                                                                                                                                                       /note="heat-labile enterotoxin A signal
212. .787
/product="heat-labile enterotoxin A1"
794. .931
                                                                                                                                                                                                                                                                                                                             /product="heat-labile enterotoxin A2"
165 c     186 g     285 t
                                                                                                                                                                                                                                                                                                          158.
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/db_xref="taxon:562"
158. .934
                                                                                                                                                                                                                                                                                                                     EETQNLSTIYLRKYQSKVKRQIFSDYQSEVDIYNRIRNEL"
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                                                                                                                                                                                                                pattern.
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of heat-labile
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OS Escherichia coli

PN JP 1992079898-A/1

PN JP 1992079898-A/1

PD 13-MAR-1992

PF 23-JUL-1990 JP 1990194:

PC C1201/68,C07H21/02,C07:

PC C1201/10,

PC (C12N15/31,C12R1:19),((C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R1:19),(C12N15/31,C12R
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FT
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S60731 1275 bp DNA linear BCT 29-heat-labile enterotoxin A subunit, heat-labile enterotoxin subunit [Escherichia coli, 21d, Genomic, 1275 nt].
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Danbara, H. and Abe, A.
DANBARA, H. and Abe, A.
DNA AND RNA PROBE TO SIMULTANEOUSLY DETECT VIBRIO CHOLERATE AND
ENTEROTOXIGENIC ESCHERICHIA COLI AND DETECTION OF VIBRIO CHOLERA
AND ENTEROGEXIGENIC ESCHERICHIA COLI USING THE SAME DNA AND RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
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13-MAR-1992

23-JUL-1990 JP 1990194208

DANBARA HIROFUMI, ABE AKIO

C1201/68,C07H21/02,C07H21/04,C12N15/11,C12N15/31,C12Q1/04,
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*source: clone=pKAD008;
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/db_xref="taxon:562"
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ORGANISM
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1 (bases 1 to 1275)

Inoue, T., Tsuji, T., Koto, M., Imamura, S. and Miyama, A. Amino acid sequence of heat-labile enterotoxin from centerotoxigenic Escherichia coli is identical to that strain H 10407
               heat-labile enterotoxin B subunit; LTh b subunit; heat-labile enterotoxin A subunit; LTh a subunit. Escherichia coli (strain:1032 (Enterotoxigenic)) DNA.
                                                                                           subunit, complete AB011677
Escherichia
                                                    AB011677.1 GI:3062900 heat-labile enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEMS Microbiol. Lett. 108 (2), 157-161 (1993)
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translation presented here differs from
publication; LTC A subunit"
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/protein_id="AAC60440.2"
/protein_id="AAC60440.2"
/db_xref="GI:18390349"
/tanslation="MKNITFIFFILLASPLYANGDKLYRADSRPPDETKRSGGLMPRG
/translation="MKNITFIFFILLASPLYANGDKYSTSLSLRSAHLAGQSILSGYSTYY
HNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILSGYSTYY
ITVIATAPNNENUNDYLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnkvkcyvLfTALLSSLCAYGAPQSITELCSEYRNTQIYTINDk
ILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="heat-labile enterotoxin B subunit"
/protein_id="AAC60441.1"
/db_xref="GI:408996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGDSSRTITGDTCN
EETQNLSTIYLRKYQSKVKRQIFSDYQSEVDIYNRIRNEL"
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Submitted (07-MAR-1998) Katsuhiro Komase, The Kitasato Institute,
Center for Basic Research, Lab. of Virology; Shirokane 5-9-1,
Minato-ku, Tokyo 108-8642, Japan (E-mail:komase-k@kitasato.or.jp,
Tel:+81-3-3444-6161, Fax:+81-3-3444-6637)
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Escherichia coli heat-labile enterotoxin with a trace amount of the holotoxin as a influence amount of the holotoxin as a
                          A16419.1
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91. .867
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/protein_id="BAA55726.1"
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/translation="MNKVKCYVLFTALLSSlcaygapqs"
/translation="MNKVKCYVLFTALLs
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REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITDDTCN
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HNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILSGYSTYY
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/protein_id="BAA25725.1"
/db_xref="GI:3062901"
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/strain="1032 (Enterotoxigenic)"
/db_xref="taxon:562"
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(., Suzuki,Y., Nagamine,T.,
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1 SerLeuArgSerAlaHisLeuAlaGlyGln
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Sequence
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                                                                                                                                                                                                                   Domenighini,M., Rappuoli,R., Pizza,M. and Hol,W. Immunogenic detoxified mutants of cholera toxin and of the toxin LT, their preparation and their use for the preparation of vaccines Patent: US 5149919-A 5 21-NOV-2000;
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/db_xref="GI:641009"
/db_xref="GI:641009"
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AGFPDPHQAMREEPMHHAPQGCGDSSRTITGDTCNEETQNLSTIYLREYQSKYKRQI
FSDYQSEVDIYNRIRDEL"
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/db_xref="taxon:562"
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Escherichia coli
Bacteria; Proteobacteria; gamma subdivisio
Escherichia.
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Chases 1 to 777)
Maikuru,B.H., Suteilbun,H. and Goodon,U.R.
MICROBIAL METHOD
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V00275 J01604
V00275.1 GI:41339
Patent: JP 1986005097-
GLAXO GROUP LTD
OS Escherichia coli
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J. Biol. Chem. 257 (10), 5716-5721 (1982)
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                                                     JP 1986005097-A 1 10-JAN-1986;
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/trans1_table=11
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/product="enterotoxin subunit A"
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/db_xref="GI:41340"
/db_xref="SWISS-PROT:D66717"
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/db_xref="taxon:562"
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                                Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, L., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, L., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Dopen, A.L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Daper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Lander, R., Lan
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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hypothetical: No;
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         Hawes, A.,
Hernandez,J.
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COMMENT

runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.

and the accession number will

1 1779 1879 3072 3172 4672 4772

1878: 3071: 3171: 4671: 4771:

ig of 1778 bp in length
of unknown length
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of unknown length
og of 1500 bp in length
of unknown length
of unknown length
of of 1661 bp in length
of unknown length

contig gap of contig

gap of contig gap of contig gap of

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

B QΥ

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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.

Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:19310258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H. Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wileczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Direct Submission
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Assembly program: phrap; version 0.990329
Consensus quality: 115361 bases at least Q40
Consensus quality: 118979 bases at least Q30
Consensus quality: 122104 bases at least Q20
                                                                                                                                                                                                                Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye:
                                                                                                                                                                                                                                                                                                                                                                       Center project name: GTHY Center clone name: CH230-398M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
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Query Match:
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**Nuzny, D.M., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burky, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Edarnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Hartn, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
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***, 84 unordered pieces.
AC120067
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                            AC120962
AC120962.2 GI:21902870
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/organism="Rattus norvegicus"
/organism="raxon:10116"
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7, *** SEQUENCING IN PROGRESS
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                                Hernandez, J.,
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18723:

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unknown of 1080

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length

of 1252

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of 2384 unknown

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of 1638

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53460:

of 2252 unknown

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of 3548 unknown of 4141

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unknown of 4463 unknown of 4566

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unknown of 2459 unknown of 2255

of 1569 unknown

length bp in l length bp in l

of 3014 unknown of 3824 unknown of 2305 unknown of 4090

bp in l length bp in l bp in l bp in ] length

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvak, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Mahabashwari, M., Mapua, P., Martin R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mel, G., Metzker, M., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Most, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-MAY-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA (Dases 1 to 174342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 174342) Worley, K.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baylor Plaza,
On Jul 18, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 84 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are unknown.

This record will be updated with the finished sequence
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be
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                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 111889 bases at least Q40
Consensus quality: 118225 bases at least Q30
Consensus quality: 122144 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                      Center project Information
Center project name: GWWD
Center clone name: CH230-27017
                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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  Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Gupten,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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Mus musculus, clone MGC:29285 IMAGE:3985822,
BC021349
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                                                                                                                                   Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Contact:
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IMAGE:3156304,
                         NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                               Strausberg,R
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     Direct Submission
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian Submitted (21-MAR-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Genomics 
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Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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STLINAALKKLDYTYLISILKDMRQNSVPVNEVVVRQLEEAAEYPPTFDRYKGKNTYL
EKIDGERAYKKMLKAMPAEEAPHPMQEFQNKPYGDQDTTDKAGGLRDG"
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old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
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/note="Voo":
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/protein_id="AAH21349.1"
/db_xref="GI:18204169"
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/db_xref="taxon:10090"
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Helobdella stagnalis.
Helobdella stagnalis
Eukaryota, Metazoa; Annelida; Clitellata; Hirudinida;
Rhynchobdellida; Glossiphoniidae; Helobdella.
                                                                                                                                        partial cds.
U10336
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This clone was selected for full length sequencing because it
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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/protein_id="AAH04766.1"
/protein_id="AAH04766.1"
/db_xref="Gi:13435831"
/translation="MKKRDLEPSDATYTALFNVCAESPWKDSALQSALKLRQQLQARN
FOLNLKTYHALLKVAAKCADLERLCLDVFKEIIQGEAPATEETFCFLLVGCIODKKTGF
ROAMQVWRQMLSIGIKPSRHGYNLLLEAARDCGLGDPEVASRLLLTTSQEEUILLPPPK
GRHMAGRKVQAKTVHGVSLRHVEALERQLFLEBSQKLEGPPALPEARVTSRTQPEVET
TAEPGHTVALTPLAPKPTHLELEVSLLSLGTLSPAVVSFGTVATPADRLALMGGLEGF
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STLINAALKKLDYTYLISILKDMRQNSVPVNEVVVRQLEFAAEYPPTFDRYKGKNTYL
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ductal carcinoma. 5 month old virgin mouse.
/clone_lip="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                   GI:520512
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/tissue_type="Mammary tumor_C3(1)-Tag model.
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/db_xref="taxon:10090"
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Yersinia pestis KIM
                                                                                                                   AE013887
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Sidow, A. and Thomas, W.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 4011)
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                                                                                        pestis KIM section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVNKMTRRDTEITKDEIMNILMYLPGWAGKLPÓPÄILKPRALWTGKOLFSIIIPGRIN
VIRTHSTHEDDEDRGPHKWISPGDTKYLVEDGKLLSGILCKKSJGASSGSLOHIIHHE
LGSDATADEYAYIOMETHWILLYTGHTIGIADTIADAKTYSDIOTAIKKAKSDVVEVI
EKAHNDELEPWEGNTLKOTFENOVNRILNDARDKTGSLAQKSLSEFNNEKSMYVAGSK
GKINISOVIACVGOONVEGKRIPFGFRORTLPHFIKDDYGPESRGFVENSYLAGLTP
TEFFFHAMGGREGLIDTAVKTAETGYIORRLIKAMESVMYKYDGTVRNOIEQLIQLRY
GEDGLAGEWEEGONLEKKPSNKAFETGYIORRLIKAMESVMYKYDGTVRNOIEQLIQLRY
GEDGLAGEWEEGONLEKKPSNKAFETGYIORRLIKAMESVMYKYDGDIKKSLNDDANVI
AEVESEYKQLLEDRTAIRQIFPSGDSKIVLPCNLQRLIWNAQKIFRIHTRKPSNLHPV
KHILDURELSKKEMIVKGEDBLSKTANTNATLLMNILVRSTLCSKRVLEEFHLSTEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AITRHGINRQETGVLAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPMLRIDQVGVPRSIAQNLTFPEIVTPENIERLTELVKRGANQYPGAKFILRETGDRI
DLRYHPKSTDLHLQFGYRVERHMQDNDYVIFNRQPTLHKMSMMCHRVKILPWSTFRLN
LSVTTPYNADFDGDEMNLHLAQSLETRAEISQLASVKRMIITPQANRPVMGIVQDSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKTKNOMKRROGFVYDLCKVETSCGGGEIDKKDDDNDHDNIKVOVGCGRHOPKIRRNL
LELTAEWKOINDDNOEKKMILTAERVLEIFKAITDETCTILGMOPKYARDEVLIATML
PVPPLPVRPAVVMFCSAKNODDLTHKLADIIKINNOLKRNEMKGAAHILLAEDTKMLO
FHVATMIDNEMPGLFRATOKSGRPLKSIKORLKGKEGRIRGNLMGKRVDFSARTVITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RNA polymerase II, largest subunit"
/protein_id="AA50227.1"
/db_xref="GI:520513"
/translation="HIELSKPVFHVPFFTKIIKILRCYCYYCSKLLIDPNHPKYKDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLQGITSIAKYYMQQPTTDDKKRIIIDEKGEFKALQDWILETDGTALRRVLSVENVDP
VKTVSNDIVEVFEVLGIEAVRKSIEREMNNVISFDGSYVNYRHLALLCDVMTAKGHLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKEIINVSKKPRAPSLTVILIGQPARDAEKAKDVLCQLEHTTLRKVTENTAIYYDPDP
MHTLIEEDQEWVYIYYDMPDVDISRLSPWLLRVELDRKRMTDKKLTMEQISEKITAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degenerate oligos (external to the sequence shown) from first strand cDNA. See Reference 1 for details"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDDLNCIFNDDNAEKLVLRVRLMSNQDGKQDQDTEEQIDKMPDDTFLKHIESNMLTDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWLMGEIESKFIQARVQPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Sequence obtained by PCR amplification with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Helobdella stagnalis"
/db_xref="taxon:34588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="early embryos"
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100.00%
53.33%
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8.00
                                            GI:21959739
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Conservative:
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                                                                                          of the complete genome
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REFERENCE
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JOURNAL
PUBMED
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-FEB-2002) Genetics, Use Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deng, W., Burland, V., Plunkett, G. III, Boutin, A., Mayhew, G. Liss, P., Perna, N. T., Rose, D.J., Mau, B., Zhou, S., Schwartz, Fetherston, J.D., Lindler, L.E., Brubaker, R.R., Plana, G.V., Straley, S.C., McDonough, K.A., Nilles, M.L., Matson, J.S., Blattner, F.R. and Perry, R.D.
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J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yersinia pestis KIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 9968)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; macromolecule degradation: Degradation of proteins, peptides, glyco"
/note="residues 12 to 271 of 308 are 25.00 pct identical to residues 3 to 247 of 283 from GenPept;
>9b|AAD36886.1|AE001819_9 (AE001819) ftsH protease activity modulator HfIC [Thermotoga maritima]"
                                                                                                                                                                                                                                                                  acids, amines"
/note="residues 10 to 252 of 252 are 78.60 pct identical to residues 1 to 243 of 243 from E. coli K12: B0860; residues 4 to 252 of 252 are 77.51 pct identical to residues 12 to 260 of 260 from GenPept: pplhAG55239.1|AE005267, 4 (AE005267) arginine 3rd transport system periplasmic binding protein [Escherichia coli 0157:H7 EDL933]"
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sydsyonaiidlkngridgvfgdtavvnewlktnpnlasvgehvtdpoyffgtglgiav
                                                                                                                                                            /product="arginine 3rd transport binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKWGKVVAVAEPGLGFKIPITEVETISISNSIKYDRLKAYSKDQOPAQMVVSIGFQ
VPPTSVEDLFVKYGSIQMMAERLVSRHYDFOVENVFGOYTAVSAYQNREDEVRKYTEE
LRKVLKDEPLIINSVNIENLDFTEGYBASIEERMKAEVUVEKTRKMLETEKINADIA
EQARGQSESQLSIAKIGAEKIKLMGAAEAENIRLMGAAEAEAIKLRADALKQNPLLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative ftsH proteinase
/protein_id="AAM86394.1"
/db_xref="GI:21959740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(214. .1140)
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                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LITAEKWNGELPQTMLPNSSVPFINARNKDGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="hflc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="hf1C"
/note="y2843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:187410"
                                                                                                           /protein_id="AAM86395.1"
/db_xref="GI:21959741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="transport; transport of small molecules; amino
acids, amines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="artJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTMKKEMSMRFVTVCGFLAILTLIAVICLMGSWYTINESDRGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="KIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Yersinia pestis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene≖"artJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72844"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  macromolecule degradation: Degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Wisconsin,
                                                                                                                                                                                           system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity modulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayhew, G.F.,
Schwartz, D.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayhew, G.F.,
                                                                                                                                                                                        periplasmic
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                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                               CDS
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complement(4031. .4495)
/gene="y2846"
/gene="y2846"
/gene="42846"
/gene="y2846"
/note="residues 6 to 142 of 154 are 42.44 pct
residues 14 to 152 of 162 from E. coli K12 : B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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/function="putative"
/note="residues 1 to 372 of 376 are 74.73 pct identical to
/note="residues 1 to 372 of 375 from E. coli K12: B0859;
residues 1 to 372 of 376 are 75.53 pct identical to
residues 1 to 372 of 375 from GenPept:
-ygb|AAG55235.1|AE005266_14 (AE005266) putative enzyme
[Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4620. .5465)
/gene="potI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residues 1 to 142 of 154 are 42.36 pct identical to residues 4 to 147 of 157 from GenPept : >emb|CAD05320.1| (AL627268) putative membrane protein [Salmonella enteric subsp. enterica serovar Typhi]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2817.
/gene="y2845"
acids, amines"
/note="residues 18 to 318 of 321 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="munipevrsywrrviltvgytflyapmimiviysfnssklytvw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="residues 1 to 280 of 281 are 84.28 pct identical to residues 1 to 280 of 281 from E. coli K12: 80857; residues 1 to 280 of 281 are 85.0pct identical to residues 1 to 280 of 281 from GenPept : >gblAAL19816.1| (AE008737) ABC superfamily (membrane), putrescine transporter [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
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/gene="y2845"
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fisbslorwbrgliffasivlllldmmcgvavchrrnwarwyvlicqliimiyllmas
                                                      /function="transport; transport of small molecules; amino acids, amines"
                                                                                                                                                  /gene-"potH"
                                                                                                                                                                                                                   complement(5462.
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/note="y2848"
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/gene="potG"
/function="transport; transport of small molecules;
acids_amines"
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GEIFALLGASGGGKSTLLRMLAGFEQPTQGGITLDGQDLSHVPPYRPFINMMFQSYAL
FPHMTVEQNIAFGLKQDKLESNEIKSRVAEMLTLVHMQEFAKRKPHQLSGQRQRVAL
RSIAKRPKLLLLDEPMGALDKKLRDRMQLEVLDILERVGATCVMVTHDQEEAMTMAG
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FLLFMLPFLIVEKISLAEMVRAVPPYTDLTTWLDGKLDISLILGUYLLLLLDDPLYIDA
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VEAALDLGARPFKTFISVIIPLTKGGIVAGSMLVFIPAVGEFVIPELLGGPDSIMIGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLSVKAEQAAFNVRRNKRREQEDKLPAPTRINFIFTVNE"
complement(7756. .8982)
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HPLKVDSDASVVDGVPVLVALRPEKVMLCDQVPKDGCNFAVGEVVHIAYLGDLSIYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="residues 1 to 375 of 377 are 86.40 pct identical to residues 28 to 402 of 404 from E. coli K12 : B0855"
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/protein_id="AAM86399.1
/db_xref="GI:21959745"
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/protein_id="AAM86401.1"
/db_xref="GI:21959747"
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/note="y2849"
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/note="y2851"
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/function="unknown"
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Submitted (20-MAR-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman Direct Submission (bases 1 to 36021) (bases 1 to 36021) 208, Norman,

Submitted (05-MAY-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman 73019, USA (bases 1 to 36021) Norman,

Direct Submission
Submitted (13-MAY-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman (bases 1 to 36021) Norman,

Direct Submission
Submitted (20-JUN-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman Direct Submission (bases 1 to 36021) 208, Norman,

Submitted (30-OCT-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman The University Of Oklahoma, (bases 1 to 36021) Norman,

Direct Submission
Submitted (16-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman (bases 1 to 36021) Norman,

Submitted (26-NOV-1998) Dep. The University Of Oklahoma, Direct Submission (bases 1 to 36021) Department Of Chemistry And Biochemistry, oma, 620 Parrington Oval, Room 208, Norman

Direct Submission Submitted (27-MAY-1999) Department Of Chemistry And Biochemistry, Submitted (27-MAY-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA 10 (bases 1 to 36021)

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OK 73019, USA 12 (bases 1 to 36021) Submitted (01-MAR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

Submitted (02-MAR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA Direct Submission Norman,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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TITLE
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             Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, R., Chen, Z., Chowdhry, I., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M.,
Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Krattovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, R., Luna, R., Ma, J.,
Maheahvari, M., Manus D., Martin, D., Mar
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OK 73019, USA
On Mar 1, 2000 this sequence version replaced gi:4895277.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and sing there are numerous instances of insertions, deletions halow
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Submitted (27-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Normar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide polymorphisms in the overlapping regions below. AC004461(119f4) 38146 44873 (0) overlaps AC004462(18c3) 1 6728 (29293) AC004462(18c3) 35015 36021 (0) overlaps AC004471(111f11) 1
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AC130257.1 GI:22164885
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Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
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norvegicus clone CH230-414I4,
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/db_xref="taxon:9606"
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4, *** SEQUENCING IN PROGRESS
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Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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Direct Submission
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moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunck, J., Bowle, S., Brieva, M., Brrown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Colwedhy, I., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
                                                                                                                                                                                                                                                                                             AC111766
AC111766.2 GI:21736856
                                                                                                                                                                                                                                                                                                                       AC111766 72519 bp D. Rattus norvegicus clone CH230-12122, ***, 37 unordered pieces.
                                                                                                                                                                                               Rattus
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30117: contig of 1472 b
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32310: contig of 2093 b
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33826: contig of 1416 b
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35868: contig of 1942 b
35968: gap of unknown 1
359176: gap of unknown 1
39176: gap of unknown 1
43139: gap of unknown 1
41339: contig of 1963 b
41339: gap of unknown 1
45088: contig of 3749 b
45188: gap of unknown 1
45080: contig of 3749 b
45187: contig of 3749 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martinez,E.,
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On Jul 12, 2002 this sequence version replaced gi:18701608
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Direct Submission
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Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez
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                                                                                                                                                                                                    (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 38289 bases at least Q40 Consensus quality: 41688 bases at least Q30 Consensus quality: 44356 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Center clone name: CH230-12I22
Center clone name: Statistics
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1003: contig of 1003 bp in length 1103: gap of unknown length 2183: contig of 1080 bp in length
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All-osman, F.R., Allen, C., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, R.C., Bred, J.R., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchlik, L., Byrd, N.C., Cleveland, C.D., Caxter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Devis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delyado, O., Denn, A.L., Ding, J., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugar-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Edwards, C.C., Elhaj, C., Escotto, M., Edwards, C.C., Elhaj, C., Escotto, M., Edwards, C., Hart, M., Halloway, C., Hollins, B., Homsi, F., Homas, F., Hart, M., Halloway, C., Hollins, B., Homsi, F., Homas, F., Hart, M., Halloway, C., Hollins, B., Homsi, F., Homas, F., Homas, F., Homas, F., Hart, M., Halloway, C., Hollins, B., Homsi, F., Homas, F., Homas, F., Hart, M., Hallow, N., Lucier, R., Lulyk, S., Hernandez, J., Homsi, F., Hollins, B., Lewis, L.C., Lewis, L., L., Lucier, R., Lucier, R., Luna, R., Ma, J., Lu, W., Lucier, R., Martindale, A., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity:
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Rattus norvegicus
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/clone="CH230-12122"
15658 c 15483 g 18574 t
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                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-JUL-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (15-MAR-2002) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jul 14, 2002 this sequence version replaced gi:19482300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 73691 bases at least Q40
Consensus quality: 74751 bases at least Q30
Consensus quality: 75325 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: GTKJ
Center clone name: CH230-105P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Project Information
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                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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48916:
                                                                                                              72259: gap of
81938: contig
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                                                                                                                          Dutchwaite, N. J., Diaper, H., Dugan Rocha, S., Dutch, N. J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gablsi, A., Gac, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, R.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R. J., Lu, X., Lucier, R., Luna, R., Ma, J.,
Mahbeshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Mansey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Oyuen, N.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Put, L.L., Quilles, M., Ren, Y.,
Sondergren, E., Sonaike, T., Sparks, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, K., Thomas, S.,
Ward, Moore, S., Warren, R., Washngton, C., Watlington, S.,
Wulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
Unpublished
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L7, *** SEQUENCING
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Worley, K.C.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 83292)
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Center clone name: CH230-328D17
Center clone name: CH230-328D17
Center clone name: CH230-328D17
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of rea Assembly program: Phrap; version 0.990329
Consensus quality: 5508 bases at least Q40
Consensus quality: 61281 bases at least Q30
Consensus quality: 64903 bases at least Q20
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
                                                                                                                       Rattus norvegicus.
Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, Tanana varsion replaced (
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 85022)
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Direct Submission
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Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisl,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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On Jul 19, 20
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                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                 Jul 19, 2002 this sequence version replaced gi:20976436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 85022)
                                                                                                                                             Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 44173 bases at least Q40 Consensus quality: 47255 bases at least Q30 Consensus quality: 49138 bases at least Q20
                                                                                                                                                                                                                                          Center clone name: CH230-155L16
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Web site: htt
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Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Eenton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulay, C., Burch, P., Burkett, C., Burnell, K.L., Byrd, N.C., Cayacos, S.R., Chacko, J., Chavec, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Escotto, M., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Cseter, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Forder, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Georrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jolivet, S., Joudah, S., Katly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC105557.2 GI:21736422
HTG; HTGS_PHASE1.
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/db_xref="taxon:10116"
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71428: contig of 2671 b
71528: gap of unknown 1
74724: contig of 3196 b
74824: gap of unknown 1
74825: contig of 3531 b
78455: gap of unknown 1
81466: contig of 3011 b
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Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Walezyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., T., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18092779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-JAN-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990339 Consensus quality: 55649 bases at least Q40 Consensus quality: 59499 bases at least Q30 Consensus quality: 62770 bases at least Q20
                                                                                                                                                                                                                                                                                                    Center project name: GNEM Center clone name: CH230-223K22
                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                 Sequencing vector: Plasmid;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 1122 1222 2308 6097 6197 7292 2408 3414 3514 3513: 4814: 4914: gap of contig gap of contig gap of contig gap of gap of gap of contig contig o f unknown of 1086 of 1095 unknown of 1301 of 1121 bp in length of 1182 unknown of 1006 1036 bp in ] length bp in l length bp in length length bp in length length bp in length
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Worley, K.C.

Direct Submission

Submitted (19-FEB-2002) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Deposit of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18701377.
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On Jul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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be preserved.
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      Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunde, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Burbrooks, S.L., Amaratunde, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Burbrooks, S.L., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brown, M., Bryant, N.P., Bouck, J., Chacks, J., 
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87697: contig of 3786 bp in length
87797: gap of unknown length
93189: contig of 5392 bp in length
93289: gap of unknown length
9537: contig of 6248 bp in length.
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Direct Submission
Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S. Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 52457 bases at least Q40
Consensus quality: 55266 bases at least Q30
Consensus quality: 57254 bases at least Q20
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Center clone name: CH230-98H10
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R.
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M.,
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Bryant, N.P., Bonnin, D., Banks, T.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-JUL-2002) Human Genome Sequencing Center, Dep of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18846366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 105756)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                    as soon as it is
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 54794 bases at least Q40 Consensus quality: 58130 bases at least Q30 Consensus quality: 61124 bases at least Q20
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                                                                                                                               RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Balbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowie, S., Brown, M., Bryant, N.P., Buck, J., Bowie, S., Brown, M., Bryant, N.P., Buck, J., Bowie, C., Chev, C., Ch
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Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                        Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa, Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,
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97453: contig of 2566 b
97553: gap of unknown 1
101094: contig of 3541 b
101194: gap of unknown 1
105756: contig of 4562 b
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of MoLecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced g1:15624514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.ligsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 86463 bases at least Q40 consensus quality: 93299 bases at least Q30 consensus quality: 93219 bases at least Q20 Estimated Insert size: 70561; sum-of-contlys estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0x in Q20 bases; agarose-fp estimation
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Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gong, W., Emanuel, B.S., Collins, J., Kim, D.H., Wang, Z., Zhang, G., Roe, B. and Budarf M.L.
A transcription map of the DiGeorge and velo-cardio-faminimal critical region on 22q11
Hum. Mol. Genet. 5 (6), 789-800 (1996)
                                                                                                    Rattus
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 1, 2002 this sequence version replaced gi:21953916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 108551)
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 62 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1053: contig of 1053 bp in length

* 1154 2241: contig of 1088 bp in length

* 2242 2341: gap of unknown length
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Best Local Similarity:
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                                                   Allen,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Cavroor,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Chen,G., Chen,R., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., David,R.L., Ding,Y.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harrie, K., Hart,M., Havlay, D., Haues, A., Herrendock, I.
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               Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J. Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 109396)
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                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This of 3 contigs. The true order of the pieces

* consists of 3 contigs. The true order of the proces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA On Jul 12, 2002 this sequence version replaced gi:18846951.
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* arbitrary. Gaps betw
* runs of N, but the e
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Center clone name: GH230-15701
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Center clone name: CH230-15701
Sequencing vector: Plasmid;
Chemistry: Dye-terminator B1g Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 68820 bases at least Q40
Consensus quality: 73510 bases at least Q30
Consensus quality: 77739 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
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of 1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pacce, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mandeshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Mettker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 78414 bases at least Q40 Consensus quality: 82108 bases at least Q30 Consensus quality: 85781 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project Information
Center project name: KBXI
Center clone name: CH230-283G2
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Chen, G., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Dalys, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Dinh, H.H., Deltaney, K.R., Deltane, K.R., Durbin, K.J., Deter, P., Frantz, P., Eagy, N., Erdwards, C., Escotto, M., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Hale, S., Hamilton, K., Harris, K., Harti, M., Havlak, P., Hawes, A., Hernandez, J., Herris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, J., Jackson, E., Klant, M., Landry, N., Lea, B., Lewis, L.C., Lewis, L.C., Kureshi, A., Landry, N., Lea, B., Lewis, L.C., Lewis, L.C., Kureshi, A., Landry, N., Leucier, R., Liu, W., Loulseged, H., Li, J., Li, M., Landry, N., Leucier, R., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Martinez, E., Massey, E., McLeod, M.P., Meador, M., Martinez, E., Michell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Owenon, G., Oragunye, N., Orledo, R., Payton, B., Peery, J., Perez, L., Petters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barsbaria,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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67 unordered pleces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Worley, K.C.
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of 1
Assembly program: Phrap; version 0.990329
Consensus quality: 29641 bases at least 040
Consensus quality: 34185 bases at least 030
Consensus quality: 38055 bases at least 020
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Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20387295
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu

Center project name: GUYS

Center clone name: CH330-354C16

Sequencing vector: Plasmid;

Chame: CH30-154C16
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Chavez, D., David, R.,

Bonnin, D., Bryant, N.P., ., Allen,C., Banks,T.,

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RESULT 40
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Query Match:
DB:
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Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvath,J., Kovar,C.,
Karlsson,E., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R., Lichtarge,O., Lieu,C., Liu,J., Liu,R., Ma,J.,
Maser,S., Manchine, J., Martin,R., Martindale,A., Martinez,E.,
Masesy,E., Mawhiney,E., Martin,R., Mardor,M., Moris,S.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Nel,L., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sundan,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Wasden,S., Wang,O.,
Wang,S., Ward-Moore,S., Warren,R., Wasden,S., Wang,O.,
Walliamson,A., Wheczyk,R., Wooden,S., Worley,K.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                            Submitted (06-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                            Submitted (18-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced g
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Direct Submission
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Direct Submission
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                                                                                                                                                              Jul 14, 2002 this sequence version replaced gi:20454688
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            Center project name: GVVF
Center clone name: CH230-402E14
----- Summary Statistics
                                                         Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                             Center code:
                                                                                                                               Center: Baylor College of Medicine
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                                                                                                                                           Genome Center
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Center, Department of Medicine, One

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Worley,K.C.
Direct Submission
Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Paza, Houston, TX 77030, USA
3 (bases 1 to 122517)
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of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
On Aug 24, 2002 this sequence version replaced gi:21953961.
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Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 58% of reads
Chemistry: Dye-terminator Big Dye: 42% of read
Assembly program: Phrap; version 0.990329
Consensus quality: 70875 bases at least Q40
Consensus quality: 76728 bases at least Q30
Consensus quality: 79150 bases at least Q20
                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 62 contigs. The true order of the pieces
is not known and their order in this sequence record is
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         Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Martin, R., Martindale, R., Mar
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Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peerry,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Rulz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Ward-Moore,S., Warren,R., Washington,C., Wactington,S., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-JUL-2002) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced g1:17974587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 124579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 124579) Worley, K.C. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 84 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 23866 bases at least Q40
Consensus quality: 26331 bases at least Q30
Consensus quality: 28175 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
------- project Information
Center project name: GJFC
Center clone name: CH230-47P11
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
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Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
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                                                                                                                                                                                                                                                                                   Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bo
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., Banks,T., Bonnin,D., Bryant, N.P.,

Allen,C.,

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AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C.
Direct Submission
Submitted (10-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 126809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C
Direct Sub
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                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of r
Assembly program: Phrap; version 0.990329
Consensus quality: 77471 bases at least Q40
Consensus quality: 80999 bases at least Q30
Consensus quality: 83473 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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/organism="Rattus norvegicus"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following absreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP attabase can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on Sep 14, 2001 this sequence version replaced gi:15131959. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-562E17 is from the library RPCI-11.2 constructed by the group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL157764
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The true right end of clone RP11-562E17 is at 137910 in this sequence. The true right end of clone RP11-217F17 is at 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-562E17 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP11-562E17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
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/clone="RP11-562E17"
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Worley K.C.

Direct Submission

Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 148879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 59 contlys. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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------ Project Information
Center project name: GMBQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
AL354740
AL354740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on Jul 25, 2001 this sequence version replaced g1:14626095. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RP11-513115 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-513115 is from the library RPCI-11.2 const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; STRISTROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[] (bases 1 to 151828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               database can be found at
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                             /note="19 copies 4 mer cctc 71% 2402. .2438 /note="MIR repeat: matches 95. .2741. .2833
                                                                                                                                               /note="MIR repeat: matches 82. .165 of consensus" 2003. .2078
                                                                                                                                                                                               /clone_lib="RPCI-11.2"
1538. .1622
                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
/note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                           /clone="RP11-513115"
                                                                                                                                                                                                                                                                                           /chromosome="6"
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21871. .2197
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                                                                                                                                                                                                 23436. .23731 repeat: matches 10.
/note="AluSx repeat: matches 1.
23732. .23759
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="13 copies 4 mer tgga 73% 21930. .21969
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15688. 15795
/note="9 copies 12 mer 79% conserved"
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4922. .5234
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/note="MIR repeat: matches 76. .235 of consensus"
3903. 3942
                                                                                                                                 /note="L1ME3 repeat: matches 5833. .6088 of consensus"
24392. .24697
                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
22774. .22866
                                                                                                                                                                                                                                                                                                                                                              /note="CpG island"
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                                                                                /note="AluJb repeat:
                                                                                                                                                                                                                                                  /note="MER5B repeat: matches 101. .171 of consensus"
                                                                                                                                                                                                                                                                                 /note="FLAM_C repeat: matches 1.
                                                                                                                                                                                                                                                                                                                  /note="MER5B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77157. .17454
/note="MER46C repeat: matches 12. .338 of consensus"
17921. .18050
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14915. .15111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="4 copies 12 mer 89% conserved"
12903. 12950
note="6 copies 8 mer gagcgagc 81% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="MER91A repeat: matches 1. .195 of consensus"
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l3560. .13621
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te="MIR repeat: matches 108.
43. .21281
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                                                                                                                                                                     7 copies 4 mer gaaa 92% conserved"
.24357
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/note="Allusx repeat: matches 151.

30292. .30593

/note="Allusg1 repeat: matches 1. .30594 .30739
                                                                                                                                                                                                                                           /note="25 copies 2 mer aa 72% conserved" 38190. 38503 /note="Aluxx repeat: matches 1. .312 of 38504. .38613
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27586 . .27736
/note="LIMC4 repeat: matches 7237 . .7390 of consensus"
27737 . .28033
                                                                                                                                                                          /note="23 copies 38619. .39430
                                                                                                                                                                                                                                                                                                                 38094. .38143
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusx repeat: matches 134.
36788. .37076
note="Alusx repeat: matches 24.
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34980. .35274
/note="AluSp repeat: matches 1. .296 of consensus'
35275. .35552
                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78638. .28816
/note="Alusg/x repeat: matches 131. .312
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28345. .28637
                                                                                                                                                                                                                                                                                                                                 note="4 copies 12 mer 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                   note-"L1M1
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36621. .36787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L1MA2 repeat: matches 2720. .3482 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MA2 repeat: matches 3482. .6110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 3.
32235. .34816
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                                                                                                                                                         Submitted (18-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TY 77030, USA On Jul 14, 2002 this sequence version replaced c
                                                                       Submitted (27-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it
be preserved
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 124262 bases at least Q40
Consensus quality: 128161 bases at least Q30
Consensus quality: 131092 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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AL Submitted (01-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Jul 23, 2000 this sequence version replaced gi:9368089.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature les ambiguous, there is an annotation using the 'unsure'
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AL355871
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:10116"
/clone="6H230-424C21"
27225 c 26942 g 49377 t
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64653 gap of unknown les
69547 contig of 4894 bp
69647 gap of unknown les
69547 gap of unknown les
69647 gap of unknown les
74136 contig of 6725 bp
81061 gap of unknown les
95126 contig of 6723 bp
95126 contig of 6725 bp
103186 gap of unknown les
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Em: EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
Waterston, R.H.
Direct Submission
Submitted (15-MAR-2000) Genome Sequencing Center, Washington
                                                                                               Direct Submission
Submitted (12-JUN-1998)
University School of Med
                                                                                                                                                                                                               2 (bases 1 to 154616)
Ryan, E., Sun, H. and Spalding, L.
The sequence of Homo sapiens PAC clone RP4-647C14
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 154616)
Sulston, J.E. and Waterston, R.
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RP11-47K11 is from the library RPGI-11.1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
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1. .154588
                                                                               MO 63108,
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Waterston, R.H.
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be approximately 1.1kb by BAMHI,
restrition enzyme digest data."
1 31281 c 29218 g 47730 t
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Medicine,
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PRP4-647C14 from 14q24.3, complete sequence.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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University, 4444 Forest
6 (bases 1 to 154616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the compact of the compac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone from chromosome 14 was provided by Roswell Park Cancer Institute, Human Genetics Carlton Streets, Buffalo NY 14263-0001 USA.
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                                                                                                                                                                                                                                                                                                                    The sequence from position 141555 product of RP4-647C14 PAC DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence RP4-647C14 contains a dinucleotide AT position 4427 to 4478. The exact number of copies
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Contact: sapiens@watson.wustl.edu
..... Summary Statistics
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                                                                                      /clone="RP4-647C14"
/clone_lib="RPCI-4"
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/chromosome="14"
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                                                                                                                                                                                                                                organism="Homo sapiens"
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Park Avenue, St. Louis,
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Missouri 63108,
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artment, Elm and
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/note="similar t
ma48g03.y1"
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4426. .44
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1187. .1330
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                             /rpt_family="Alu"
7363. .7649
                                                                                /rpt_family="Alu"
7051. .7357
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2993. .3023
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/rpt_family="Alu'
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: January 28, 2003, 12:15:22  
Job time: 1666.67 secs
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7650. .7795
n 7650. .7795
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n 8221. .8560
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1881. .9083
                                                                                                                                                                                                                                                                                                                   /rpt_family="L1"
9771. .9820
/rpt_family="L1"
9825. .9956
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/rpt_family="Alu"
10899. .11021
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9092. .9459
/rpt_family="L2"
9496. .9671
                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
10049. .10282
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Matches:
Conservative:
Mismatches:
Indels:
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Command line parameters:

MODEL-frame+_p2n.model -DEV-x1h

-MODEL-frame+_p2n.model -DEV-x1h

-Q-/Ggn2_1/USPTO_Spool_MORIN682/runat_23012003_130140_7866/app_query.fasta_1.597

-DB-N_Geneseq_101002 -OFMT-fastap -SUFFIX-olip2n.rng -MINMATCH-0.1 -LOOPCL-0

-LOOPEXY=0 -UNITS-bits -START=1 -END=-1 -MARIXIX-olip0 -TRANS-human40.cdi

-LIST-1000 -DOCALIGN=200 -THR_SOCRE-quality -THR_MIN-8 -ALIGN=50 -MODE=LOCAL

-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000

-USER-BORIN682_@CGN_1 1_187_@runat_23012003_130140_7866 -NCPU-6 -ICPU-3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7

-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 1000 summaries
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length: 2000000000
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Ygapop 60.0
Fgapop 6.0
Delop 6.0
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                                                                                                                                    1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prinand is derived by analysis of the total score distribution. being printed,

## SUMMARIES

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	л с 	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	80.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match I	
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2000	7751114	AAV81595	AAQ42768	AAQ51326	AAQ51325	AAQ51324	AAQ51323	AAQ51322	AAQ51321	AAQ51320	AAQ51319	AAQ51318	AAQ51317	AAQ51316	AAQ51315	AAQ51314	AAA51140	AAS01505	AAS01506	ABL40639	AAQ23864	ABL40640	AAA51544	AAA51147	AAA51106	AAN50206	AAN50205	ABK50864	ID	!
CITACHET SET U ECT		heat	E.coli heat labile	Encodes Lys-114 E.	Encodes Glu-114 E.	-106	104	104	104	Encodes Glu-107 E.	Encodes Tyr-97 E.c	Encodes Lys-97 E.c	Encodes Lys-63 E.c	Encodes Tyr-53 E.c	Encodes Glu-53 E.c	۹sp-	Oligomer sLT-A Rev	E. coli heat-labil		E. coli heat-labil		ᠴ			Plant-optimized E.	of the	Sequence of the pi	Escherichia coli h	Description	

## ALIGNMENTS

RESULT 1 ABK50864 ID ABK5 Escherichia coli heat labile enterotoxin sub-unit A. 30-JUL-2002 (first entry) ABK50864; ABK50864 standard; DNA; 723 BP.

Co-expression DNA vaccine; antibacterial; antiviral; antiparasitic; immunostimulant; vaccine; immune response; systemic tolerance; Tat-mediated immune deviation; ds; heat labile enterotoxin sub-unit Escherichia coli. sub-unit A.

WO200219968-A2.

14-MAR-2002.

10-SEP-2001; 2001WO-US28365

08-SEP-2000; 2000US-231070P. 08-SEP-2000; 2000US-231376P. 08-SEP-2000; 2000US-231403P. 08-SEP-2000; 2000US-231449P.

(UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

Hone D, Shata M, Lewis G, I Agwale S; Fouts 'n Bagley K, Boyson ĭ Obriecht

ü

WPI; 2002-383031/41.

Co-expression DNA vaccines comprising an antigen-encoding region and a

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Best Local Si
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ1-65T079 (1-15) x ABK50864 (1-723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                     CDS
                                                WPI; 1985-148358/25
P-PSDB; AAP50190.
                                                                                                                                                                                                                                                                                          E.coli NCIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inducing significantly stronger immune responses against vaccine antigens than conventional DNA vaccines, and are also capable of inducing systemic tolerance. This sequence represents the Eschericali heat labile enterotoxin sub-unit A that up-regulates CAMP let The enterotoxin is an immunoregulatory molecule useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         active component such as adjuvants, immunoregulatory peptides and proteins, antisense RNAs, and catalytic RNAs. The co-expression DNA vaccines are useful for vaccinating animals against viral, bacterial and parasitic pathogens, for enhancing immune responses, for inducir systemic tolerance, and for treating and/or preventing Tat-mediated immune deviation. The co-expression DNA vaccines are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a new DNA vaccine comprising a region encodi an antigen component and a region encoding at least one biologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biologically active component-encoding region, useful as vaccines against viral, bacterial and parasitic pathogens, or for enhancing
                                                                                                                                                               12-DEC-1984;
                                                                                                                                                                                        19-JUN-1985
                                                                                                                                                                                                                EP145486-A
                                                                                                                                                                                                                                                                                                                Pig scours vaccine;
                                                                                                                                                                                                                                                                                                                                        Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 723 BP; 238 A; 128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 89; 108pp; English
                       New toxoid as inactivated form of toxin for
                                                                                                             (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                 30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                          AAN50205;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAN50205 standard;
                                                                                                                                       12-DEC-1983;
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          from organism transformed by gene
                                                                                       Harford
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                                                                                                                                                                                                                                                                                                                                        the pig
                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA vaccines described in the
                                                                                                                                       83GB-0033131
                                                                                                                                                              84EP-0308620
                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                toxin; diarrhoea;
                                                                                                                                                                                                                                                                                                                                        scours
                                                                                     Ross
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                                                                                                                                                                                                                                                                                                                                                                                                                   777
                                                                                                                                                                                                                                                                                                                                       heat labile toxin (LT) LTA gene
                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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XXCCCCCXX
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN50205 is the gene sequence of the natural LTA gene. The LTA ge the site directed mutant SDM1 (see AAN50206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional K antigens opt. with whole cells component the antigens opt.
                                                                                                                                                                                                                                                                                        CDS
                                                             Example; Fig 2; 61pp; English
                                                                              New toxoid as inactivated obtd. from organism trans
                                                                                                            P-PSDB;
                                                                                                                     WPI; 1985-148358/25
                                                                                                                                       Hayes MV,
                                                                                                                                                                           12-DEC-1983;
                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                  E.coli NCIB
                                                                                                                                                                                                                                                                                                                                   Pig scours vaccine;
                                                                                                                                                                                                                                                                                                                                                      Sequence of the pig scours site directed mutant SDM1.
                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                    AAN50206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                        (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                             12-DEC-1984;
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                                                                                                                                                                                                                                  EP145486-A.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAN50206 standard;
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                                                                                                             AAP50191
                                                                                                                                      Harford S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig
                                                                                                                                                                                                                                                                                                                   11932
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                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                           83GB-0033131
                                                                                                                                                                                             84EP-0308620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; 61pp;
                                                                                                                                                                                                                                                                    /*tag= a
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/note= "TCC
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                                                                                        form of toxin
                                                                                                                                                                                                                                                                                                                                    diarrhoea;
                                                                                                                                                                                                                                                                                                                                                               heat labile toxin (LT) LTA gene of the
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                                                                                                                                        GW.
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Matches:
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                                                                                         for use
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                                                                                         vaccines
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AANSO205 is the gene sequence of the natural LTA gene. The LTA gene the site directed mutant SDMI (see AANSO206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the

of

inactivated LTA.

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
This plant-codon optimized cDNA encodes a synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The sequence contains plant-preferred codons and eliminates sequence mottifs associated with spurious mRNA processing. A single codon insertion (CTG encoding valine) was made to accompdate the creation of a NcoI restriction site around the was made to accompdate the creation of a NcoI restriction site around the polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the
                                                                                            New polynucleotides encoding LT-A transformation of plant cells, use elicit immune responses in animals
                                                                                                                               P-PSDB;
                                                                                                                                                                       (BOYC-)
(MASO/)
(ARNT/)
                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                 Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
adjuvant; anti-bacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA51106 standard; cDNA; 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                              WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000
                                                                            Example 1; Fig 1; 103pp; English.
                                                                                                                                        WPI; 2000-442653/38.
                                                                                                                                                       Mason HS, Arntzen CJ,
                                                                                                                                                                                                                            22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                 Escherichia
                                                                                                                                                                                                          22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AGTTTGAGAAGTGCTCACTTAGCAGGACAGTCTATATTATCAGGA
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                                                                                                                                                                       BOYCE THOMPSON INST PLANT MASON H S. ARNTZEN C J.
                                                                                                                               AAY96646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777
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57..779
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                                                                                                             LT-A or
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                                                                                                      useful
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                    CT-A polypeptides for the in immunogenic composition
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AAA51147
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         Example
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (CT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adjuvant; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 782
elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                        mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA51147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA51147 standard; cDNA;
           New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositi
                                                                                                                                                                                                            22-DEC-1998;
                                                                                                                                                                                                                                            22-DEC-1999;
                                                                                                                                                                                                                                                                            29-JUN-2000.
                                                                                                                                                                                                                                                                                                          WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000
                                                                                                                                                           (BOYC-) BOYCE THOMPSON INST PLANT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AGCTTGAGGTCTGCTCACTTGGCAGGACAATCCATCCTCTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-442653/38
                                                                                                               NS,
                                                                                                                                               ARNTZEN
                                                                AAY96647
                                                                                                            Arntzen CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                           heat-labile_toxin-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA51544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants. Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A cDNA shown in AAA51106 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accommodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or
                                         22-DEC-1998;
                                                                                                       29-JUN-2000
                                                                                                                                   WO200037609-A2
                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                          adjuvant; anti-bacterial; R192G; ss.
                                                                                                                                                                                                                                                                                                                                                                                     Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant-preferred codons and eliminates sequence motifs associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A subunit (LT-A). The codon at nucleotide positions 246-248 was changed from the wild-type TCC to AAG which causes a change of serine to lysine in the mature protein at residue 63. The sequence contains
(MASO/) MASON
                                                                       22-DEC-1999;
                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                           Heat-labile toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA51544 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes a mutant S63K Escherichia coli heat-labile toxin (LT) (LT-A). The codon at nucleotide positions 246\text{-}248 was changed
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
THOMPSON INST PLANT RES
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3..59
                                           98US-0113507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
                                                                                                                                                                                                                                                                                                                                                      LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                                                                                                                                    coli LT-A G192 mutant coding sequence
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                      ABL40640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mature protein at residue 192. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A colory polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of the mutant polypeptides are also useful as adjuvants.

Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A cDNA shown in AAA51106 which is constructed from the wild type LT-A cDNA shown in AAA51106 which is
                                  misc_feature
                                                                                                                                   Escherichia
                                                                                                                                                                   vaccine;
                                                                                                                                                                                 LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant;
                                                                                                                                                                                                                  E. coli mutant heat-labile toxin (mLT) 5B-SD-1A protein encoding DNA
                                                                                                                                                                                                                                                    17-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A subunit (LT-A). The nucleotide at position 631 was changed from the wild-type A to G which causes a change of arginine to glycine in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
                                                                                                                                                                                                                                                                                    ABL40640
                                                                                                                                                                                                                                                                                                                    ABL40640 standard; DNA; 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                      252
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                                                                                                                                                                                                                                                                                                                                                                                                  SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly
                                                                                                                                                                                                                                                                                                                                                                                      AGCTTGAGGTCTGCTCACTTGGCAGGACAATCCATCCTCTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-442653/38.
                                                                                                                                                                   mutant;
                                                                                                                                    coli
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B₽;
             /*tag=
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/note= "contains an internal
                                                                                 Location/Qualifiers
1..1143
/note=
                                                                                                                                                                   mLT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 A; 186 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a mutant R192G Escherichia coli heat-labile toxin (LT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.00%
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 "mLT 5B subunit"
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RESULT 8
AAQ23864
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a gene encoding a protein having a subunit structure of IA5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene)-(SD sequence gene)-(A subunit gene). A method is provided for the preparation of a protein having a subunit structure of IA5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli mutant heat-labile toxin (mLT) 5B-SD-1A protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 12-13; 27pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of a protein having 1A5B structure
                                                                                    LTh; STla; STlb; t probe; detection;
                                                                                                                        Thermolabile toxin (LTh) gene
                                                                                                                                                  08-OCT-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-299402/34. P-PSDB; ABB07785.
          13-MAR-1992
                                    JP04079898-A
                                                             Esherischia coli.
                                                                                                                                                                               AAQ23864;
                                                                                                                                                                                                       AAQ23864 standard; DNA; 1148 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1143 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG 2000; 2000JP-0238740
                                                                                                                                                                                                                                                       07-AUG-2000; 2000JP-0238740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EB-2002
                                                                                               thermolabile; heat-stable; E.coli; T4DNA ligase;
                                                                                      SS
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07-AUG-2000; 2000JP-0238740

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RESULT 9
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Thermolabile toxin (LTh) gene sequence is derived from enterotoxigenic E. coli. An LTh-ST12.STMD probe, wherein all all or part of the sequences of the Wingertoxin genes represented in AAQ23864-66 are ligated toreach owner by T4DNA ligase, may be used for the detection of VMDSMORROTERA and enterotoxigenic E.coli simultaneously in a simple way. The method has the same sensitivity as the dangerous radio-isotope
                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                              19-FEB-2002.
                                                                                          misc_feature
                                                                                                                         misc_feature
                                                                                                                                                       misc_feature
                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                         LT; heat-labile toxin; vaccine; ds.
                                                                                                                                                                                                                                                                       E. coli heat-labile toxin (LT) 5B-SD-1A protein encoding DNA.
                                                                                                                                                                                                                                                                                             17-JUN-2002
                                                                                                                                                                                                                                                                                                                  ABL40639;
                                                                                                                                                                                                                                                                                                                                       ABL40639 standard; DNA; 1152 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1148 BP; 399 A; 205 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-1990;
                                                  JP2002051779-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-137930/17
                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Obe 1807 Simultaneous defection of Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90JP-0194208
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                                                                                                                                                       /note= "contains an internal SD sequence"
1..312
                                                                                        /*tag= c
/note= "SD sequence"
340..1152
                                                                                                                         /note= "LT 5B
313..339
                                                                                                                                                                                       Location/Qualifiers
1..1152
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                                                                      "LT
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                                                                      1A subunit"
                                                                                                                                   subunit"
                                                                                                                                                                                                                                                   toxin; CT;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                    recombinant; adjuvant;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a gene encoding a protein having a subunit structure of 1A5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene) - (SD sequence gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coll heat-labile toxin (LT) 5B-SD-1A protein encoding DNA.
  15-SEP-1999;
                             15-SEP-1999;
                                                                                        WO200119998-A1
                                                                                                                                                                                                                                                                         Heat-labile enterotoxin; LT; LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; Gs. endotoxin; diarrhoea; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1152 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2000; 2000JP-0238740
                                                                                                                                                                                                                                                Escherichia coli strain K88ac
                                                                                                                                                                                                                                                                                                                                  E. coli heat-labile enterotoxin (LT) mutant LTdell10/112 DŅA
                                                                                                                                                                                                                                                                                                                                                              29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                           AAS01506;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAS01506 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 AGTTTGAGAAGTGCTCACTTAGCAGGACAGTCTATATTATCAGGA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly 15
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)B; ABB07784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOKURITSU GYOSEI
HIGETA SHOYU KK.
FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                              (first
                             99WO-KR00555
                                                                                                               /product= "LTdell110/112 mutant protein"
/trans1_except= (pos:932..933,aa:Met)
/note= "This codon has an apparent 1 nu
deletion which alters the readin
                                                                                                                                                                                       164..1305
                                                                                                                                                                                                      Location/Qualifiers
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Groups of mice were immunised with LTS623Y or LTdell10/112. The control groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunised with LTS63Y or LTdell10/112 contained high and comparable level of anti-LT antibodies in sera and faecal extracts compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LTS637 blocks NAD-binding. Deletion of Glu residues at positions 110 and 112 in LTdell10/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein the regulates CAMP levels. The resulting increase in CAMP is the cause of diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LTS637 and LTdell10/112 were tested.
                                                                                                              Escherichia Synthetic.
                                                                                                                                                                               detoxified
                                                                                                                                                        Headenianalle enteration; LT, LTS63Y; LTdeli10/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; Gs; endotoxin; diarrhoea; ds.
                                                                                                                                                                                                                                                                                                   AAS01505;
                                                                                                                                                                                                                                                                                                                                 AAS01505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1508 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adjuvant for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxin (LT) mutant LTdell110/112. LTS63Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 45-46; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful as vaccine for preventing for antibody production
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                                                                                                                                                                                                                                coli heat-labile enterotoxin (LT) mutant LTS63Y
                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                               coli strain K88ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence encodes for Escherichia coli heat-labile
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/*tag= a
/product= "LTS53Y mutant protein"
/transl_except= (pos:938..939,aa:Met)
/note= "This codon has an apparent 1:
                                                                              Location/Qualifiers
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                                                                                                                                                                              RESULT 12
AAA51140/c
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                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes for Escherichia coli heat-labile centerotoxin (LT) mutant LTSG3Y LTSG3Y and LTGell10/112 (AAU00507) are two novel detoxified and immunologically active proteins (LT cutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LTSG3Y blocks (NAD-binding. Deletion of Glu residues at positions 110 and 112 in CTGell10/112 eliminate the enzymatic activity of LT. The Al subunit of twild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that cregulates cAMP levels. The resulting increase in cAMP is the cause of CC diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of Groups of mice were immunised with LTSG3Y and LTGell10/112 were tested. CC Groups received phosphate buffered saline (PBS) alone. The serum and CC faecal antibody titres to LT were determined. The results showed that CC comparable level of anti-LT antibodies in sera and faecal extracts are useful as a vaccine for preventing and treating diarrhoea and as an antibody production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant for antibody production .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park EJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1514 BP; 510 A; 277
                          Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; adjuvant; anti-bacterial; ss.
                                                                        Oligomer sLT-A Rev-14 for LT-A cDNA synthesis
                                                                                                                                                              AAA51140 standard; DNA;
                                                                                                      26-SEP-2000
                                                                                                                                                                                                                          1 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly 15
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Matches:
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Escherichia coli

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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC Oligonuclectide 40-mers (AAA51107-26) spanning the entire synthetic CC Escherichia coli heat-labile toxin (LT) A subunit (LT-A) coding sequence CC and a set of complementary 40-mers (AAA51127-46) that centre on the CC junctions of the coding oligomers allowing 20 bp overlaps were obtained CC commercially and used to construct the synthetic LT-A cDNA. The sequence CC contains plant-preferred codons and eliminates sequence motiffs CC encoding valine) was made to accommodate the creation of a Ncol CC encoding valine) was made to accommodate the creation of a Ncol CC polynuclectides encode a mutant LT-A polypeptide or a mutant vibrio CC cohlerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have CC reduced enzyme activity as compared to the wild-type LT-A or CT-A CC polypeptide and where at least one of the codons is altered to a plant CC preferred codon. The polynucleotide further comprises a nucleic acid CC sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The CC polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially CC oral vaccines in transgenic plants for the prophylactic or therapeutic CC treatment against E. coll or V. cholerae. The mutant polypeptides are useful as adjuvants.
                                                                                                                                                                     AAQ51314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOYC-) BOYCE THOMPSON INST PLANT RES (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions
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                                                                                    08-DEC-1993
                                                                                                                    AAQ51314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40 BP;
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                                                 Encodes Asp-53 E.coli heat labile toxin subunit A.
                                                                                                                                                   AAQ51314 standard; DNA; 711
                                                                                                                                                                                                                   (first entry)
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                       The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51314 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                   enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
protomer A; site-directed mutagenesis; reduced toxicity;
ADP-ribosyltransferase activity; ss.
                                                                                                                    08-DEC-1993
             Escherichia coli
                                                                                         Encodes Glu-53 E.coli heat labile
                                                                                                                                            AAQ51315;
                                                                                                                                                                    AAQ51315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                  235 A;
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                                                                                         toxin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                  G,
                                                                                                                                                                                                                     219
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                                                                                                                                                                                                                                                                                                                                                                                                  198 T;
                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
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RESULT 15
AAQ51316
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                                                                                                                                                                                                                                                                                                                                  Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                    misc_difference 153..155
                                                                                              enterotoxigenic bacteria; vaccine; imm
protomer A; site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenic, detoxified LT-A proteins and their use in vaccines protect against enterotoxigenic E.coll. Sequence AAQ51315 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al. J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-051326). The invention relates to
                                                             Escherichia
                                                                                     ADP-ribosyltransferase
                                                                                                                                   Encodes Tyr-53 E.coli heat labile toxin subunit A.
                                                                                                                                                            08-DEC-1993
                                                                                                                                                                                                            AAQ51316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae an enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                              NO...
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOC-) BIOCINE SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09313202-A
                                                                                                                                                                                                                                                           190
                                                                                                                                                                                                                                                                      1 SerLeuArgSerAlaHisLeuAlaGlyGln
                                                                                                                                                                                                                                                           AGTTTGAGAAGTGCTCACTTAGCAGGACAG
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DB; AAR38731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                            standard;
                                                             coli
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                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 153..155
/note= "wild-type GTC(Val) mutated to TAC(Tyr)"
              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                 236 A; 122 C;
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                                                                                                                                                                                                            DNA;
                                                                                    activity;
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                                                                                               vaccine; immunogenic detoxified LT-A;
mutagenesis; reduced toxicity;
                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 156 G;
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Matches:
Conservative:
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Indels:
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RESULT 16
AAQ51317
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AC AAQ51
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Best Local Similarity:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51316 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                   enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
  08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                   Encodes Lys-63 E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ51317 standard; DNA;
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                                                         WO9313202-A
                                                                                                                                                                   misc_difference
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DB; AAR38732.
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                                                                                                                                                                Location/Qualifiers 184..186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 A; 123 C; 155 G; 198 T; 0 other;
                                                                                                         /note= "wild-type TCT(Ser) mutated to AAG(Lys)"
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                          detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                   toxicity;
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RESULT 17
AAQ51318
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic, detoxified LT-A proteins and their use in vaccines t protect against enterotoxigenic E.coli. Sequence AAO51317 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                  enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                  AAQ51318 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 711 BP;
                                           08-JUL-1993.
                                                                 WO9313202-A.
                                                                                                            misc_difference
                                                                                                                                              Escherichia coli
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                     30-DEC-1992;
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                      92WO-EP03016
                                                                                                                                                                                                                E.coli heat labile toxin subunit
                                                                                                            Location/Qualifiers 277..279
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                                                                                       /*tag=
/note=
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                                                                                      "wild-type GTT(Val)
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Matches:
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                                                                                        mutated
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31-DEC-1991;

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KESULT 18
AAQ51319
 Percent Similarity:
Best Local Similarity:
Query Match:
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Domenighini M,
                                                                         30-DEC-1992;
                                                                                                08-JUL-1993
                                                                                                                                                                      misc_difference
                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected t site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                31-DEC-1991;
                                                                                                                        W09313202-A
                                                                                                                                                                                   Key
                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                  Encodes
                                                                                                                                                                                                                                                                                                                                 AAQ51319;
                                                                                                                                                                                                                                                                                                                                                         AAQ51319 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 711 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protect against enterotoxigenic E.coli. Sequence AAQ51318 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino
                        (BIOC-) BIOCINE SCLAVO SPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numbering is based on the cholera toxin A subunit sequence)
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DB; AAR44017.
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                                                                                                                                                                                                                                                                               Tyr-97 E.coli heat labile toxin subunit
                                                                                                                                                                                                          coli.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                91IT-0MI3513
                                                                        92WO-EP03016
Hol W,
                                                                                                                                                                    Location/Qualifiers 277..279
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/note= "wild-type GTT(Val) mutated
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Pizza M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 G; 196 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
Rappuoli
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ1-65T079 (1-15) x AAQ51319 (1-711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (ramamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51319 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                       WPI; 1993-227320/28
                                                                                                                      30-DEC-1992;
                                                                                                                                                08-JUL-1993.
                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                   ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                enterotoxigenic bacteria;
protomer A; site-directed
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                                                                                                                                                                                                                                                                                                                                                                                                            AAQ51320 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae ar
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P-PSDB; AAR44018.
                                              Domenighini M,
                                                                     (BIOC-) BIOCINE SCLAVO
                                                                                                31-DEC-1991;
                                                                                                                                                                        WO9313202-A
                                                                                                                                                                                                                                                                                                                                                            08-DEC-1993
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                                                                                                                                                                                                                                                                                                                                   Glu-107 E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                            coli.
                                                                                                                                                                                                                                                                                               enic bacteria; vaccine; immunogenic
site-directed mutagenesis; reduced
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                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                91IT-0MI3513
                                                                                                                       92WO-EP03016
                                              Hol
                                                                                                                                                                                                                     Location/Qualifiers 307..309
                                                                                                                                                                                             /note= "wild-type CAC(His) mutated to GAG(Glu)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 A; 124 C;
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Matches:
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Mismatches:
                                             Rappuoli
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RESULT 20
AAQ51321
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Pred. No.:
Score:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                   enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
        Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
            enterotoxin
                                                                                                    Domenighini M,
                                                                                                                                                        31-DEC-1991;
                                                                                                                                                                                30-DEC-1992;
                                                                                                                                                                                                         08-JUL-1993.
                                                                                                                                                                                                                                                                                       misc_difference
                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                         Encodes Lys-104 E.coli heat labile toxin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ51321 standard; DNA; 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic - useful as
                                                                                                                              (BIOC-) BIOCINE
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                                                               1993-227320/28.
DB; AAR44020.
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51321 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                          Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae an enterotoxin producing Escherichia coli
The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic detoxified
protomer A; site-directed mutagenesis; reduced toxicity;
                                      Claim 3; Fig
                                                                                                                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993
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                                                                                                                                                      Domenighini
                                                                                                                                                                                                         31-DEC-1991;
                                                                                                                                                                                                                               30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encodes Asp-104 E.coli heat labile toxin subunit A.
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                                                                                                                                                                               (BIOC-) BIOCINE
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DB; AAR44021.
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                                      2 and Page 46;
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yanamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51322 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence)
                                                                                      Claim
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protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                            enterotoxin
                                                                                                                        Immunogenic - useful as
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                                                                                    Fig
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                                                                                                          detoxified mutant cholera toxin and heat labile toxin vaccines against infection by Vibrio cholerae and producing Escherichia coli
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                       The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al., J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected is site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ53314-051326). The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protect against enterotoxigenic E.coli. Sequence AAQ51323 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amin acid numbering is based on the cholera toxin A subunit sequence.)
         protect against enterotoxigenic E.coli. Sequence AAQ51324 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amir
                                                                                                                                                           Immunogenic detoxified mutant - useful as vaccines against i enterotoxin producing Escheric
                                                                                                                                                                                                                                                                                                                         30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ51324;
                                                                                                                                      Claim
                                                                                                                                                                                                                                                  Domenighini M,
                                                                                                                                                                                                                                                                          (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                   31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                            WO9313202-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enterotoxigenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encodes Ser-106 E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ51324 standard; DNA;
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                                               immunogenic,
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DB; AAR44023.
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                                                                                                                                    3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                                                                            nic detoxified mutant cholera t
as vaccines against infection
xin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                               detoxified LT-A proteins and their use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                   91IT-0MI3513
                                                                                                                                                                                                                                                  HO1
                                                                                                                                                                                                                                                                                                                          92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 304..306
                                                                                                                                                                                                                                                                            SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "wild-type CCT(Pro) mutated
                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 A; 122 C; 157 G; 198 T; 0 other;
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Matches:
Conservative:
Mismatches:
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o cholerae an
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primer sequence used to introduce the pacid numbering is based on the cholera

toxin A subunit sequence)

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                                 The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51325 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino et al. 2015) and the mutagenic control of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ51325
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Sequence
                                                                                                                                                                  Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                     31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encodes Glu-114 E.coli heat labile toxin subunit A.
                        primer sequence used to introduce the pacid numbering is based on the cholera
                                                                                                                                                                                            enterotoxin
                                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                               P-PSDB; AAR44024.
                                                                                                                                                                                                                                                                                    Domenighini M, Hol
                                                                                                                                                                                                                                                                                                                                                               30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                            (BIOC-) BIOCINE SCLAVO SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosyltransferase activity; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
 711
                                                                                                                                                                                           producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli.
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 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "wild-type TCT(Ser) mutated
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236 A;
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 122 C;
                                                                                                                                                                                                                                                                                    Pizza
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 157 G;
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Matches:
Conservative:
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 196
                         toxin A subunit sequence)
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 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detoxified
toxicity;
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Alignment Scores:

Best Local Similarity:

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RESULT 2:
AAQ51326
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                      Score:
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Best Local Similarity:
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           Percent Similarity:
                                                                                The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected toxic strain mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51326 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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                                                                                                                                                                                                                       enterotoxin
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                                                               Sequence
                                                                                                                                                                                                                               Immunogenic - useful as
                                                                                                                                                                                                                                                                                            Domenighini M,
                                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                        31-DEC-1991;
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                                 NO . .
                                                                                                                                                                                                 Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                      detoxified mutant cholera toxin and heat labile toxin vaccines against infection by Vibrio cholerae and producing Escherichia coli
                                                                                                                                                                                                 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                            92WO-EP03016
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Matches:
Conservative:
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                                                               <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxin subunit
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Best Local Similarity:
                             SEQ1-65T079 (1-15) x AAQ42768 (1-711)
                                                              Query Match:
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DB:
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                                                                                                                                                   of a strain of E.coli known to affect humans. The sequence was published by Yamamoto et al. J.Biol. Chem., 259, 5037-5044. Mutations at selected positions within this sequence have been for reduce toxicity (see AAQ51314-Q51326). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines protect against enterotoxigenic E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                   Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                        enterotoxin
                                                                                                     No.:
                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                               WPI; 1993-227320/28.
P-PSDB; AAR38728.
                                                                                                                                                                                                                                                                                                                             Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                    31-DEC-1991;
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         SerLeuArgSerAlaHisLeuAlaGlyGln 10
                                                                                                                                                                                                                sequence encodes the A subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTTGAGAAGTGCTCACTTAGCAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuArgSerAlaHisLeuAlaGlyGln
711 BP;
                                                                                                                                                                                                                                                      producing Escherichia
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                                                                                                                                 234 A; 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; immunogenic detoxified LT-A;
                                                                                                                                 C;
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                                                                                                                                 156 G; 198
                                                                              Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                       coli
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                                                                                                                                                                                                                                                                                                                           Rappuoli
                                                            Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reduced toxicity;
                                                                                                                                 Ŧ,
                                                                                                                                                                                                    heat labile toxin (LT-A)
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                                                                                                                                                                                                                                                 prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with the antigen in the compositions and a pharmaceutically acceptable carrier. The antigen may be derived from viruses, bacteria, parasites and fungi or may be tumour antigens, self-antigens and allergens. The compositions are therefore useful in the treatment and prevention of
                                                                                                                          e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites), AIDS, autoimmune diseases (e.g. Systemic Lupus Erythematosus), Alzheimer's disease and cancers The adjuvant can also be used to prepare antibodies against selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one selected uncay. (optionally topical) vehicle. The adjuvant composition with at least one antigen in administered parenterally in conjunction with at least one antigen in the adjuvant has the ability and the adjuvant has the ability of the adjuvant has the adjuvant h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected antigen e.g. in disease treatment
Sequence 711 BP;
                                                                                               antigen(s), useful e.g. for diagnostic purposes or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methods to immunise vertebrate subjects. The adjuvant has the abilit to enhance the humoral and cell-mediated immune responses elicited by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence corresponds to the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1A-B; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-070064/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1998;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parenteral adjuvant; antigen; antigen; immunisation; humoral
cell-mediated immune response; virus; bacterium; parasite; fu
tumour; allergen; pathogen; AIDS; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E. coli heat labile toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV81595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i heat labile toxin, an example of a bacterial ADP-ribosylating
A mutant detoxified form of this protein is used in a parenteral
t composition, which comprises the detoxified protein, at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW67772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Del Giudice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erythematosus; Alzheimer's disease; diagnosis;
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97US-0041227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP-ribosylation; mutant; detoxification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region for the A subunit of the
                                                                                               antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungus;
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Alignment Scores:

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Length:

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Best Local Similarity: Query Match:
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                                    Oligonucleotide 40-mers (AAA51107-26) spanning the entire synthetic CC Escherichia coli heat-labile toxin (LT) A subunit (LT-A) coding sequence CC and a set of complementary 40-mers (AAA51127-46) that centre on the CQ junctions of the coding oligoners allowing 20 bp overlaps were obtained CC commercially and used to construct the synthetic LT-A cDNA. The sequence CC contains plant-preferred codons and elininates sequence motifs CC associated with spurious mRNA processing. A single codon insertion (GTG CC encoding valine) was made to accommodate the creation of a NCOI CC restriction site around the initiator methionine codon. Novel CC polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio CC cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have CC reduced enzyme activity as compared to the wild-type LT-A or CT-A CC polypeptide and where at least one of the codons is altered to a plant CC sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The CC production of transgenic plants to produce edible vaccines, especially craftment against E. coli or V. cholerae. The mutant polypeptides are area of the codons are septial or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ1-65T079 (1-15) x AAV81595 (1-711)
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                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligomer sLT-A For-8 for LT-A cDNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA51114 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BOYC-) BOYCE THOMPSON INST PLANT RES.
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adjuvant; anti-bacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful as
                               adjuvants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0113507
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Sequence

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Best Local Similarity:
                              SEQ1-65T079 (1-15) x AAA51114 (1-40)
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Search completed: January Job time: 345.333 secs 28, 2003, 10:56:27 DЪ

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/BORIN682/runat_23012003_130141_7880/app_query.fasta_1.597
-DB=EST -QFMT=fastap -SUFFIX=ollp2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=olligo -TRANS=human40.cdi -LIST=1000
-DOCALION=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXELN=200000000
-USER=BORIN682_@CGN_1_1_1349 _@runat_23012003_130141_7880 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
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Sequence:
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seq length: 2000000000
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ygapop 60.0,
Fgapop 6.0,
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gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	ult No.	Score	Query Match	Length	BB	ID	Description
	-	8	53.3	263	17	AZ788524	
O	N	8	53.3	418	9	AI347100	
O	ω	8	53.3	424	17	AQ786225	
	4	œ	53.3	454	12	BE744213	
	ъ	80	53.3	490	17	AQ209383	
C	σ	8	53.3	503	12	BF443144	
ဂ	7	œ	53.3	535	13	BI343334	
	8	8	53.3	615	17	вн329082	
O	9	8	53.3	646	12	BG824614	
	10	89	53.3	648	17	AZ403745	
.,	11	8	53.3	706	13	BI090511	
	12	8	53.3	725	17	вн271552	
	13	80	53.3	735	17	вн351398	
O	14	80	53.3	768	13	BI658656	
	15	œ	53.3	790	17	CNS03A1W	
ဂ	16	8	53.3	816	17	AQ745347	
O	17	8	53.3	829	17	CNS03WYZ	
ი	18	8	53.3	870	12	BF120183	
ი	19	8	53.3	884	12	BF575766	
	20	80	53.3	967	17	CNS03N3Z	
ဂ	٥	,	53.3	1877	11	BC019121	

## ALIGNMENTS

RESULT 1 AZ788524 LOCUS JOURNAL COMMENT FEATURES REFERENCE SOURCE ORGANISM KEYWORDS VERSION ACCESSION DEFINITION TITLE AUTHORS source Tel: Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 263)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. 263 bp DNA linear GSS 16 2M0035K08R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0035K08 R, DNA sequence. Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: | Plate: 0035 row: K column: 08 Seg primer: CACACAGGAAACAGCTATGACC High quality sequence stop: Location/Qualifiers Unpublished (2000) plasmid inserts Mouse whole genome scaffolding with paired end reads from 10kb Mus musculus Tel: 801 585 5606 Fax: 801 585 7177 A2788524.1 nouse mouse. lass: plasmid ends USA /organism="Mus musculus" /strain="C57BL/6J" /db\_xref="taxon:10090" /clone="UUGC2M0035K08" GI:12928413 0.00 Bldg., 20 S 2030 GSS 16-FEB-2001 genomic SLC, T.

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SEQ1-65T079 (1-15) x AZ788524 (1-263)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 418) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI347100 418 bp mRNA linear EST 30-DEC-1998 qp55a12.xl NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926910 3' similar to TR:015498 O15498 SNARE PROTEIN YKT6.;, mRNA sequence.
                                           High quality sequence stop: 1.
Location/Qualifiers
                                                                                                           Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                      Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                          primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."

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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                       High quality sequence stop: 424 Location/Qualifiers
                                                                                                                                                                                                                                                                      Seq primer: T7
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RESULT 2 AI347100/c

DEFINITION

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BASE COUNT

Score

No : :

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/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1926910"
/clone_lib="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                            Length: Matches:
                           Indels:
                                               Mismatches:
                                                                        Conservative:
418
8
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AV/86225 424 bp DNA linear GSS 03-AUG-1999 HS\_3137\_Al\_All\_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=21 Row=A, DNA sequence. AQ786225 GSS 03-AUG-1999

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 424)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Sequence-tagged connectors: A sequence approach to mapping Keller,A., Shaker,R., Furlong,J., Young,J., ing the human genome Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) Zhao,S., Adams, M.D. and and

Contact: Mahairas GG, Wallace JC, Seattle, Hood WA 98109,

REFERENCE AUTHORS

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION

COMMENT

JOURNAL TITLE

FEATURES

Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3137 row: A column: 21

/organiam="Homo sapiens" /ob\_xref="taxon:9606"=" /clone="plate=3137 Col=21 Row=A" /clone\_lib="CIT Approved Human Genomic Sperm Library D"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 1 76 c 83 g 144 t 1 others

ORIGIN

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REFERENCE
AUTHORS
TITLE
JOURNAL
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/tlssue_type="adenocarcinoma cell line"
/tlssue_type="adenocarcinoma cell line"
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/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_2: xhoI; Site_2: xhoI;
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/db_xref="taxon:9606"
/clone="IMAGE:3838221"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, He High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                  BF443144
260525 MJ
BF443144
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 503)

FahrenKrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                            pig.
Sus scrofa
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E-Coli DH10B"
a 113 c 99 g 146 t
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/clone="Plate=3240 Col=16 Row=I"
/clone_110="CIT Approved Human Genomic Sperm Library
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                                                                                 USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366
Fax: 402 762 4390
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Single pass sequencing. Bases ov
v0.980904.e. Vector identified
                                                                                                                                                    Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries EST discovery in swine
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Fahrenkrug, S.C., Fr
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                               Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
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and Keele, J.W.
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Sus scrofa
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smith@email.marc.usda.gov
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cass_match with the -minscor
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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                                                                                                                                                                                                                   Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH329082 615 bp DNA linear GS CH230-105P11.TJ CHORI-230 Segment 1 Rattus norvegicus CH230-105P11, DNA sequence.
BH329082
                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Shetty,J., Shatsman,S., ',A., Gebregeorgis,E., Overton,L., Jong,P. and Fraser,C.M.
                                                                                                                     Seq primer: SP6
Class: BAC ends.
                                                                                                                                                             (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 105 row: P column: 11
                                                                                                                                                                                                                                                                                                                                               Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_GSSs: CH230-105P11 TVB
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                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat
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301 838 0208
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/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-105P11"
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/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db_xref="taxon:9823"
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, Russell,D., Chen,D.,
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; Murinae;
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Best Local Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG824614.1 GI:14172201
EST.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information cafond through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Plate: LLCM1737 row: o column: 12
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                                                                                                             /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
.58 a 172 c 168 g 148 t
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
171 c 170 g 186 t
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4868195"
/clone_lib="NIH_MGC_15"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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648 bp DNA linear GSS 03-OCT-200
IM0171010R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0171010 R, DNA sequence.
AZ403745
AZ403745.1 GI:10527758
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University of Utah
Rm. 308, Biomedical
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Unpublished (2000)
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Mammalia; Eutheria;
1 (bases 1 to 648)
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Insert Length: 10000 Std Error: (
Plate: 0171 row: 0 column: 10
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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            125
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                           musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/clone="UUGC1M0171010"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo l (bases 1 to 706)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BI090511.1 GI:14508841
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60285511F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4996971 5',
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Location/Qualifiers
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Plate: LLAM11023 row: e column:
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                                                                                                                                                                                                                                                                     /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                     /Clone="IMAGE:4996971"
/Clone_lib="NIH_MGC_10"
/Cell_line="MGC36"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                              GSS.
Rattus norvegicus
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SEQ1-65T079 (1-15) x BH271552 (1-725)
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Best Local Similari
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                                    вн351398 вн351398.1
                                                                       BH351398 735 bp
CH230-175A4.TJ CHORI-230 Segment 1
CH230-175A4, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
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Mammalia; Eutheria; Rodentia;
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BH271552.1 GI:17183954
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Class: BAC ends.
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Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pTARBAC2.1; Site_1: EcoRI; CHORI-230 Rat (BN/SSNHSd/MCW) BAC library Pieter de Jong" a 163 c 181 g 266 t
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/clone="CH230-34M7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
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                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                            BI658656
BI658656.1 GI:15572892
                                                                                                                                                                                                                                            BI658656 768 bp mRNA linear EST 12-SEP-2001 603283613F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5328074 5',
 Email: cgapbs-r@mail.nih.gov
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 768)
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
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Other_GSSs: CH230-175A4.TV
                                                                                                                                           Mus musculus
                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                 mRNA sequence.
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Fax: 301 838 0208
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment
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CHORI-330 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
171 c 182 g 265 t
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/clone="CH230-175A4"
/clone_11b="CHORI-230 Segment 1"
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SEQ1-65TO79 (1-15) x BI658656 (1-768)
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Roest-Crollius, H., Jaillon, O., Dasily
Bouneau, L., Billault, A., Quetier, F.,
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished 3 (bases 1 to 790)
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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/clone="IMAGE:5328074"
/clone_11b="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
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Bernot,A. and
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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816 bp DNA linear GSS 16-JUL-1999
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sapiens genomic clone Plate=2276 Col=21 Row=C, DNA sequence.
A0745347
                                                                                                                                                                                                    Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2276 row: C column: 21
                                                                                                                                                                                                                                                                   401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 816)
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Class: BAC ends
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Natl. Acad. Sci. U.S.A. 96 (17),
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/note="Genoscope sequence ID : COBG
/note="Organ: sperm; Vector: pBeloBAC11; BAC
E-Coli DH10B"
                                                                  /clone="Plate=2276 Col=21 Row=C"
                                                                                                    /organism="Homo sapiens"
                                   /sex="male"
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Submitted (12-APR-2000)
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Bernot, A., Fizames, C., Wincker, P., Brottier, P.,
Saurin, W. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
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BASE COUNT
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BF575766/c
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                                                                     DEFINITION
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mRNA sequence.
BF575766
BF575766.1 GI:11649478
EST.
                                                                 BF575766 884 bp mrNA linear EST 12-DE 602135396F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290670
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAW9190 row: a column: 23
High quality sequence stop: 651.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BF120183
BF120183.1 GI:10959223
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: Not1; Cloned unidirectionally. Primer: Oligo di Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3985822"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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SOURCE
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Best Local Similarity:
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lini.gov

Plate: LLCM1133 row: o column: 23

High quality sequence stop: 486.

Location/Qualifiers
Roest-Crollius,H., Jaillon,O.,
Bernot,A., Fizames,C., Wincker,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                       AL251576.1 GI:7972588
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis genome survey sequence T7 end of c 0.39 \times 0.5 of library G from Tetraodon nigroviridis, genomic
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                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
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Homo sapiens
                                                                      (bases 1 to 967)
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/db_xref="taxon:9606"
/clone="IMAGE.4290670"
/clone="IMAGE.4290670"
/clone="ID="NIH_MGC_81"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant); Vector: pDNR-LIB
/(note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: Sfi1 (ggccgcttgggc); Site_2: Sfi1
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTACAGGCCGAGCGGCGCGACATG-dT(30)BN-3' (where B = A,
C, G, or T). A Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonles contained
inserts by PCR. This library was enriched for full-length
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                                              Dasilva, C., Bouneau, L., Fisher, C.,
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                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus, clone IMAGE:5002987, mRNA.
BC019121
BC019121 GI:17403065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N. Ayele,K. Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                              Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                 Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using 
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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/note="Genoscope sequence ID : C0BG039AF03LP1-end : T7"
1 203 c 245 g 246 t 1 others
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Search completed: January 28, Job time: 1272.67 secs
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                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                Best Local Similarity:
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                                                                                       353 AGCCTGAGGTCTGCACACTTGGCG 330
                                                                                                             1 SerLeuArgSerAlaHisLeuAla 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 39 Row: C Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identity to protein
This clone has the following problem: no 5'
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         473
                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor. M. old mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam2" /lab_host="DHIOB" /note="Vector: pcMV-SPORT6" a 504 c 525 g 375 t
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5002987"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation TITLE OF INVENTION: Their Use for the Preparation of Vaccines NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

and

APPLICANT:

Pizza, Mariagrazia

ADDRESSEE: Chiron STREET: 4560 Hortc CITY: Emeryville STATE: California

4560 Horton Street

Chiron Corporation

California

```
GenCore version 5.1.3 Compugen Ltd
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 28, 2003, 10:38:10 : Search time 54 Seconds (without alignments) 85.188 Million cell updates/sec

Sequence: Perfect score: SEQ1-65T079 SLRSAHLAGQSILSG

Scoring table: Xgapop 60.0 Ygapop 60.0 Fgapop 6.0 Delop 6.0 OLIGO . . . . Xgapext Ygapext Fgapext Delext 60.0 60.0 7.0 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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-LIST-1000 -DOCALIGN-200 -THR\_SCORE-quality -THR\_MIN-8 -ALIGN-50 -MODE-LOCAL
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Database : Issued\_Patents\_NA: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

_	Result
10	sult Query No. Score Match Length DB ID
10 66.7	Query Match
711	Length
ω	BB
711 3 US-08-823-120-5	lesult Query NO. Score Match Length DB ID Description
Sequence 5, Appli	Description

# ALIGNMENTS

RESULT 1 US-08-823-120-5 Sequence 5, Application US/08823120 Patent No. 6149919 GENERAL INFORMATION: APPLICANT: Domenighini, Mario Rappuoli, Rino

> δÃ Best Local Similarity: Query Match: Search completed: January 28, 2003, 13:19:48 SEQ1-65TO79 (1-15) x US-08-823-120-5 Alignment Scores: US-08-823-120-5 Job time : 54 secs Percent Similarity: TELEFAX: (510 (655-3542)
> INFORMATION FOR SEQ ID NO: 5:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 711 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: DNA (genomic) CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION UMMBER: US 08/256
> APPLICATION UMMBER: US 08/256
> FILING DATE: 11-NOV-1994
> ATTORNEY/AGENT INFORMATION:
> NAME: MCCLUNG, Barbara G.
> REGISTRATION UMMBER: 33,113
> REFERENCE/DOCKET NUMBER: 0315
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (510) 601-2708
> TELEFAX: (510) 655-3542
> TELEFAX: (510) 655-3542 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/823,120 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk FEATURE: No. : 190 AGTTTGAGAAGTGCTCACTTAGCAGGACAG 219 FILING DATE: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COUNTRY: USA ZIP: 94608-2916 LOCATION: NAME/KEY: 1 SerLeuArgSerAlaHisLeuAlaGlyGln 10 DNA (genomic) 0.0182 10.00 100.00% 100.00% 66.67% US 08/256,003 0315.001 (1-711)Gaps: Length: Matches: Mismatches: Indels: Conservative: 711 0 0 0

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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-MODEL-frame+_p2n.model -DEV=xlh
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Sequence 5, Appli
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ALIGNMENTS

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Percent Similarity:
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Query Match:
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Search completed: January 28, 2003, 13:23:11 Job time: 63 secs
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                                                                                                                                                                                                                                                                                         ; LENGTH: 723
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-950-335A-5
                                                                                                                            SEQ1-65TO79 (1-15) x US-09-950-335A-5 (1-723)
                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENETICANT: HONE, DAVID M.
APPLICANT: HONE, DAVID M.
TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTIO
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 4115-128
CURRENT APPLICATION NUMBER: US/09/950,335A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09950335A Publication No. US20020193330A1
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                                                             1.4e-07
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Matches:
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Indels:
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Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-Q-/cgn2_1/USPT0_spool/BORIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-DB-GenEmbl -QFMT=fastap -SUFFIX-olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-oligo -TRANS-human40.cdi -LIST=1000
-DCCALIGN=200 -THR_SCORE-quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL -OUTEMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN-2000000000
-USER-BORIN682_GCGN_1_1_2425_grunat_23012003_130141_7873 -NCDU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARRI_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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285.757 Million cell updates/sec
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enterotoxin; heat-labile enterotoxin.
E.coli (strain SA53) DNA.
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Genetics of type IIa heat-labile enterotoxin of Escherichia coli:
operon fusions, nucleotide sequence, and hybridization studies
J. Bacteriol. 169 (11), 5180-5187 (1987)
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E.coli heat-labile
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Pickett, C.L., Weinst
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QLKKYIADVNTNTRGIYVVSNTGGVWYIPGGRDYPDNFLSGEIRKTAMAAILSDTKVN
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YRGDLFRGLTYAPNEDGYQLAGFFSNFPAMREMPWSTFAPEGCVPNNKEFKGGVCISA
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/protein_id="AAA24094.1"
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/db_xref="taxon:562"
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                                                                                                                                  /note="heat labile enterotoxin type IIa
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AL Submitted (17-Nov-2001) Wellcome Trust Sanger Institute, Hinxton, Submitted (17-Nov-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 30, 2001 this sequence version replaced gi:16304764.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ValProAsnAsnLysGluPheLysGly 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-100P23 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 229289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt SWISSPROT;\ Tr:,\ TREMBL;\ wp:,\ WORMPEP;\ Information\ on\ the\ WORMPEP\ database\ can\ be\ found\ at\ }
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                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP23-100P23.
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/note="Single clone region. Sequence from clone PCR only." 170770. .170774 /note="1327 bases of IS2 transposon (V00610) removed here. This sequence represents the duplicated flanking sequence
                                                                                                            /note="Sequence from uni-directional dGTP big dye terminator reads only." 125096. 125397
                                                                                                                                                                                                          59782.
                                                                                                                                                                                                                              /clone="RP23-100P23"
/clone_lib="RPCI-23"
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/chromosome="11"
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/note="Sequence from uni-directional dGTP big dye terminator reads only."
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-Dbs-N_Geneseq_101002 -QFWT=fastap -SUFFIX=011P2n.rng -MINMATCH=0.1 -LOOPCL=0
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-NO_XLPXY -NO_MMAP -LAGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query No. Score Match Length DB ID

Description

No matches found

Search completed: January 28, 2003, 10:56:27 Job time: 344.333 secs

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	SUMMARIES
NO.	Overy Description Description
ь	8 53.3 683 10 BB016585 BB016585 BB016585
	ALLGNMENTS
RESULT 1 BB016585	
DEFINITION	BD016585 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930563A03 3', mRNA sequence.
ACCESSION VERSION	BB016585.2 GI:16257466
SOURCE	use.
	Chordata: Crantata: Vertebrata:
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  1 (bases 1 to 683)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishli,Y., Ito,M., Kawai,J., Konno,H., Kouda
	A., Nomura,K., Ohno,M., i,C., Sakai,K., Sano,H., S ki.T., Sogahe,Y., Suzukit,
9 1 9 1 9 1	Tagami,M., Tagawa,A., Takanashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. DTERN Moneo Ecce (Arabana d. ct. al. 2001)
JOURNAL	
	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic
	Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
	Tel: 81-45-503-9222 Fax: 81-45-503-9216
	Emall: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carrinci p Shibata v Havatsu N Sugabara v Shibata k Itob
	,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
	genes. Genome Res 10 (10), 1617-1630 (2000)  want K Futiwako S Troug K Torawa V Trawa M Ohara F
	Watchiki, Yongda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
	<pre>Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format</pre>
	<pre>pipeline with 384 multicapillary sequencer. 757-1771 (2000)</pre>
	Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a
	Honredundant Cuwa Libidiy. Genome Res II (2), 201-209 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa .K. Fukuda,S. Hara A. Itoh M. Kawai,I. Shihata K. and
	Hayashizaki,Y. Communitational Analysis of Full-Length Mouse CDNAs Commared with
	equences Mamm. Genome. 12, 673-677 (2001) our web site (http://genome.gsc.riken.go.jp/)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: January 28, 2003, 13:16:52 Job time : 1270.67 secs
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                                  Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                             /sex="male"
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Search completed: January 28, 2003, 13:19:48 Job time : 54 secs
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-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=Olip0 -TRANS=human40.cdi
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-NO_XLPXY -NO_MMP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPPOP=60 -YGAPEXT=60 -DELEXT=7
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-MODEL-frame+_p2n.model -DEV-xlh
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Maximum DB seq length: 2000000000
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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-DEV_TIMEOUT=120 -WARM_TIMEOUT=30 -THREADS=1 -XCAPOP=60 -XCAPEXT=60 -FGAPOP=6
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Fgapop 6.0 , Fgapext 7.0
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// Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
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Copyright (c) 1993 - 2003 Compugen Ltd
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Search completed: January 28, 2003, 13:23:11 Job time : 63 secs

No matches found

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-O_cgp2_1/USPTO_Spool/BORING82/runat_23012003_130141_7873/app_query.fasta_1.597
-DB-GenEmb1 -QFMT-fastap -SUFFIX-01ip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blits -START=1 -END--1 -MATRIX-01ig0 -TRANS-human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE-quality -THR_MIN-8 -ALIGN-50 -MODE-LOCAL -OUTEMT-pto
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-USER-BORIN682_@CGN_1 1_2425_@runat_23012003_130141_7873 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOXT=7
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SUMMARIES

#### Result No. Score 0,000,000,000,000,000 Query Match Length DB 55.00 1262 714035 1101445 114928 11429589 1429587 152617 154455 15334 175334 175334 10 2 2 2 2 2 2 2 2 10 ECOETOXHL AF204796S8 AC123728 AL133411 AC125479 AC025445 AL139131 AC1139131 AC0113881 AC092328 AL1390718 AL0925445 AL0925445 ij AC068609 AF204803 Mus muscu AC123728 Mus muscu AL133411 Human DNA AC125479 Medicago AC025453 Homo sapi AL139131 Homo sapi AC113881 Rattus no AC021844 Homo sapi AC023228 Homo sapi AL390718 Human DNA AC025445 Homo sapi AL390718 Human DNA AC025445 Homo sapi M28523 Escherichia Description

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CDS	-10_signal	-35_signal	gene				source	FEATURES	COMMENT	PUBMED	MEDLINE	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	ECOETOXHL	RESULT 1
113904	gnal 26. 31		/gene="LT-IIb"	/Clone="pCP4185"	/strain="41" /sh vrof="+avon-550"	/organism="Escherichia coli"		Location/Qualifiers	On Nov 28, 1994 this sequence version replaced g1:341953.	2670900	89359131	J. Bacteriol. 171 (9), 4945-4952 (1989)	IIb heat-labile enterotoxin gene of Escherichia coli	Cloning, nucleotide sequence, and hybridization studies of the type	Pickett, C.L., Twiddy, E.M., Coker, C. and Holmes, R.K.	1 (bases 1 to 1262)	Escherichia.	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	Escherichia coli	Escherichia coli (strain 41) DNA.	LT~IIb gene; enterotoxin type IIb.	M28523.1 GI:576584	M28523	(LT-IIb) A and B chain genes, complete cds.	Escherichia coli (strain 41) heat-labile enterotoxin type IIb	ECOETOXHL 1262 bp DNA linear BCT 18-NOV-1994		

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Debeljak,N., Horvat,S.,
                                                                    Pflugers Arch. 439 (3 Suppl), R7-R8 (2000)
                                                                                                     Debeljak, N., Horvat, S., Komel, R. and Rozman, D. Molecular cloning and partial characterisation
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ELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVN
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/protein_id="AAA53286.1"
/db_xref="GI:576586"
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14-alpha-demethylase (CYP51) gene, exon 9.
Vouk, K., Lee, M. and Rozman, D.
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                Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Letter, M., Marchis, N., Marchis, M., Marchis, N., Marchis, M., Marchis, N., Marchis, M., Marchis, N., Marchis, M., Marchi
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Mischier, Cone Rp23-453L19
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Mus musculus clone RP23-453L19, LOW-PASS SEQUENCE SAMPLING.
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Submitted (15-NOV-1999) Medical Center for Molecular Biology,
Institute of Biochemistry, Medical Faculty, University of
Ljubljana, Vrazov trg 2, Ljubljana 1000, Slovenia
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Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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3 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-JUN-2002) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 15, 2002 this sequence version replaced gi:21307290. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Plerre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Pollara,V., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
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Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,
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Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Y
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                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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828 1556: contig of 729 bp
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28778: contig of 730 bp 17

8878: gap of 100 bp 17

29601: contig of 723 bp 17

19701: gap of 100 bp 17

30450: contig of 749 bp 1
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348: gap of 130 bp in 13078: contig of 730 bp in 178: gap of 100 bp in 13889: contig of 711 bp in 100 bp in 1715 bp in 17
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6429: gap of 100 bp
17139: contig of 710 bp
17239: gap of 100 bp
17977: contig of 738 bp 1.
18071: gap of 100 bp
18070: gap of 723 bp 1.
18000: contig of 723 bp 1.
18000: gap of 100 bp
19633: contig of 733 bp 1.
19633: gap of 733 bp 1.
19733: gap of 734 bp 1.
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22992: contig of 737 bp 1

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23815: contig of 723 bp 1

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                                                                                                                                                                                                                 Submitted (17-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 21, 2002 this sequence version replaced gi:10931831. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                               only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT: Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
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Submitted (27-JUN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-57P14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
This sequence was finished as follows unless otherwise noted: all
                                                                                                     Shaull, S., Lin, S., Dixon, R., Cook, D., Kim, D. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC125479 GI:22297354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC125479 114928 bp DNA linear Medicago truncatula clone mth1-7f11, WORKING DRAFT
                                                                                                                                                                            Unpublished
                                                                                                                                                                                                     Medicago
                                                                                                                                                                                                                            Cook, D., Kim, D. and
                                                                                                                                                                                                                                                Shaull, S., Lin, S., Dixon, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sections only once, except for a short overlap.

The true left end of clone RP11-298E2 is at 99446 in this sequence
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RP11-57P14 It may be shorter because we sequence overlapping
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/chromosome="9"
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/clone_lib="RPCI-11.1"
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                         Room 208, Norman,
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RESULT 6
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1 3787: contig of 3787 bp in length

3788 3887: gap of unknown length

1362: la261: gap of unknown length

1362: la261: gap of unknown length

23764: contig of 10503 bp in length

23765: 23864: gap of unknown length

23765: 23864: gap of unknown length

23865: 37301: contig of 13437 bp in length

37302: 37401: gap of unknown length

37402: 51846: contig of 13445 bp in length

51947: 51946: gap of unknown length

51947: 51946: gap of unknown length

51947: 3772: gap of unknown length

73673: contig of 21726 bp in length
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On Aug 19, 2002 this sequence version replaced gi:22138503
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 142959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-AUG-2002) Department Of Chemistry And Biochemistry. The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
Unpublished
                    Sequencing of Human Chromosome
                                   DOE Joint Genome Institute.
                                                                                                                                                                             AC025453
AC025453.5 GI:13677022
                                                                                                                                                                                                                                      ACO25453 142959 bp DNA linear Homo sapiens chromosome 5 clone CTD-2150A8, WORKING
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                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                     ordered pieces.
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This sequence will be replaced
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/clone="mth1-7f11"
/clone 11b-"...
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SEQ4-65TO79 (1-15) x AC025453 (1-142959)
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Consensus quality: 141252 bases at least Q30
Consensus quality: 141950 bases at least Q30
Estimated insert size: 155560; agarose-fp estimation
Estimated insert size: 142259; sum-of-contigs estimation
Quality coverage: 5.9 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.45 in Q20 bases; sum-of-contigs
* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* the accession number will be preserved.

* This sequence will be preserved.

* 1 23816 83941: contig of 5661 bp in length
* 23716 23715: contig of 17954 bp in length
* 83942 84041: gap of unknown length
* 83942 84041: gap of unknown length
* 83943 84041: gap of unknown length
* 97948 98047: contig of 60126 bp in length
* 104250 106891: gap of unknown length
* 104350 106891: contig of 5202 bp in length
* 104350 106891: gap of unknown length
* 104350 106991: gap of unknown length
* 104350 106991: gap of unknown length
* 135030 135029: contig of 28038 bp in length
* 135030 135029: contig of 28038 bp in length
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* 135030 135029: contig of 28038 bp in length
* 135030 135029: contig of 28038 bp in length
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DOE Joint Genome Institute.
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er: Joint Genome Institute
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/db_xref="taxon:9606"
/chromosome="5"
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26024 c 25587 g 43364 t 704 other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads consensus quality: 137751 bases at least Q30 consensus quality: 142555 bases at least Q30 consensus quality: 142252 bases at least Q20 Insert size: 144882; sum-of-contigs Insert size: 156750; 4.8% error; agarose-fp quality coverage: 3.78x in Q20 bases; sum-of-contigs Quality coverage: 3.58x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2000 this sequence version replaced gi:9212172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Sanger Centre
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ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 145882)
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103697: contig of 34408 bp in length
3698 103797: gap of 100 bp
116670: contig of 12873 bp in length
571 116770: gap of 100 bp
131840: contig
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                    /clone="RP11-172P10"
/clone_lib="RPCI-11.1"
                                                                                                      /db_xref="taxon:9606"
                                                                                                                                      /organism="Homo sapiens"
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28758: gap of 100 bp
33908: contig of 5150 bp in length
34008: gap of 100 bp
37706: contig of 3698 bp in length
37806: gap of 100 bp
50897: contig of 13091 bp in length
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contig of 13942 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
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ORGANISM
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ORIGIN
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           Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Cleveland, L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dederich, D. A., Davila, M.L., Davis, C., Davila, M.L., Davila, M.L., Davila, M.L., Davila, M.L., Davila, M.L., Davila, M.L., Ding, Y., Dinh, H.H., Delaney, K.R., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Ehlaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabis, A., Garner, T., Garza, N., Gill, R., Garia, A., Garner, T., Garza, N., Gill, R., Garral, M., Garner, T., Garza, N., Garral, M., Garral, M.
                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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50998. .56577
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34072 c 34219 g
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131941. .145882
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103798. .116670
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67089. .69189
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28759. .33908
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116771. .131840
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Molecular and Human Company USA
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gl:19526054.
Genome Center
Company of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-JUI-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 118622 bases at least Q40
Consensus quality: 122734 bases at least Q30
Consensus quality: 125850 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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     1078: contig of 1078 bp in length
1178: gap of unknown length
2244: contig of 1066 bp in length
2344: gap of unknown length
4170: contig of 1826 bp in length
4270: gap of unknown length
5512: contig of 1242 bp in length
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COMMENT

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Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator B1g Dye; 0% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 152020 bases at least 040
Consensus quality: 152947 bases at least 030
                                                                                                                      Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 11, 2000 this sequence version replaced gi:7523912.
                                                                                                                                                                                                                                                                                                          2 (bases 1 to Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                  I (bases 1 to 154455) Waterston, R.H.
                                                                                                                                                                        Center: Washington University Genome Sequencing Center Center code: WUGSC
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99172: gap of unknown le
103575: contig of 400 bp
103675: gap of unknown le
112734: contig of 9059 bp
112834: gap of unknown le
119742: contig of 6908 bp
119842: gap of unknown le
129603: contig of 9761 bp
129703: gap of unknown le
138726: contig of 9023 bp
138726: contig of 13791 b
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ne 5 clone RP11-15D23, WORKING DRAFT SEQUENCE,
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Db 56862 TTTAACTCTTTGCCTAATAACAAG 56885
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              1 (bases 1 to 155394)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
Unpublished
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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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98643. .154455
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/chromosome="5"
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10735: gap of unknown length
44171: contig of 33436 bp in le
44271: gap of unknown length
9842: contig of 54271 bp in le
98642: gap of unknown length
154455: contig of 55813 bp in le
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Consensus quality: 153819 bases at least Q30
Consensus quality: 153879 bases at least Q30
Consensus quality: 153879 bases at least Q30
Estimated insert size: 16366; agarose-fp estimation
Quality coverage: 12.32 in Q20 bases; sum-of-contigs estimation
Quality coverage: 12.32 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                    sequence.
AL390718
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Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                        Direct Submission
                                                 Wallis,J
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 176123)
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/clone_lib="RPCI human BAC library 11"
28012 c 28437 g 52363 t 100 others
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/db_xref="taxon:9606"
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25917: gap of unknown length
155394: contig of 129477 bp in length
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This sequence was finished as follows unless otherwise noted: all
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184635)
DOE Joint Genome Institute and Stanford Human Genome Center.
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The true left end of clone RP11-502H18 is at 1 in this sequence. The true left end of clone RP5-1180Cl0 is at 155124 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr1 RP11-502H18 is from the library RPCI-11.2 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
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Direct
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VECTOR: pBACe3.6
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                                                                                                                                                       Homo sapiens.
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Submission
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/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-11.
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                                                       Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Tsurgeon,E.D.
                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 192263)
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HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 6, 2001 this sequence version replaced gi:10567849. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-OCT-2000) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
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/clone="CTD-2049017"
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                       5 SerLeuProAsnAsnLysAlaSer 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-OCT-2001) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA On Oct 27, 2001 this sequence version replaced gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-MAY-2000) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 192263)
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Center clone name: 098L05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: NISC Web site: http://www.nisc.nih.gov
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nucleotides 9258-10025; 768
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160265~160266
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AC068665 (nucleotides 199679-205937) clone RP23-426K16
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can be found in GenBank Accession Number AE000112.1
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/chromosome="5"
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18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1999.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1999.DAT: *
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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1999.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn-embl/Na1981.DAT:*
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Ygapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query No. Score Match Length DB ID Description

No matches found

Search completed: January 28, 2003, 10:56:27 Job time: 344.333 secs

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GenCore version 5.1.3
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1: em_esthba:* 2: em_esthun:* 3: em_esthun:* 4: em_estov:* 5: em_estcv:* 6: em_estro:* 8: em_htc:* 9: gb_est1:* 10: gb_est2:* 11: gb_est3:* 12: gb_est4:* 13: gb_est4:* 14: gb_est5.** 15: em_estfun:* 16: em_estfun:* 17: gb_est5.* 18: em_gss_hum:* 19: em_gss_hum:* 20: em_gss_fin:* 21: em_gss_fin:* 22: em_gss_mus:* 23: em_gss_mus:* 24: em_gss_mus:* 25: em_gss_other:* 26: em_gss_other:* 27: em_gss_fod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

BASE COUNT	T T FEATURES P FEATURES SOURCE	REFERENCE 1 AUTHORS K L TITLE L JOURNAL U COMMENT C	RESULT 1 BQ987313/c LOCUS DEFINITION Q ACCESSION VERSION KEYWORDS SOURCE ORGANISM S A	Result Score No. Score 1 8 C 1 8 C 2 8 C 3 8 C 4 8 C 4 8
/Clone_lib="QG_EEGHJ lettuce serriola". //clone_lib="QG_EEGHJ lettuce serriola". //lab_host="p.coli" //note="vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QG_EEGHJ lettuce serriola TAG_SEG=CGAATGCGGG"  73 g 84 t	t Davis (UCD) , CA 95616, USA chelmore@vegmail.ucdav ntigl26, see http://cg mn: 24. rs a sativa" iola"	Knapp,S., le,D., Ch. s., Livi radford,K from the .edu/ .edu/	BQ987313 BCI:22404838 EST. Lactuca sativa Lactuca sativa Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;	Query

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REFERENCE
AUTHORS
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KEYWORDS
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BQ986290/c
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nrtp://compgenomics.ucdavis.edu/
Unpublished (2002)
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Tavalla.D., Chevaller, P., Ziegle, J., Ellison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactuca sativa
Lactuca y Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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QGE9B01.yg.ab1 QG_EFGHJ lettuce
QGE9B01, mRNA sequence.
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Plate: QGE9 row: B column: 01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                belongs to contig QG_CA_Contig126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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                                                                                                                                        TAG_TISSUE=germinating seeds
TAG_SEQ=TCTGTGCGGG"
                                                                                                                                                                                         TAG_LIB=QG_EFGHJ lettuce serriola
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGE9B01"
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/lab_host="E.coli"
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BQ983106/c
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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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343 bp mRNA linear EST 21-AUG-2002 QGE18D17.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGE18D17, mRNA sequence.
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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Plate: QGE18 row: D
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
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48 c 82 a
                                                                                                                                                                                                                                                                                construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_EFGHJ lettuce serriola
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/lab_host="E.coli"
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Wed Jan 29 10:46:39 2003

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                                                        SEQ4-65T079 (1-15) x BU010453 (1-501)
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                     LeuProAsnAsnLysAlaSerSer 13
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QGJ13H21.yg.abl QG_EFGHJ L
QGJ13H21, mRNA sequence.
BU010453
BU010453.1 GI:22444848
EST.
   Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] singleton, see http://cgpdb.ucdavis.edu/ for details. plate: QGJ13 row: H column: 21.
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactuca
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                                                                                                                                                                                                                                                         /note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB-QC_EFGHJ lettuce serriola TAG_TISSUE-flowers pre-fertilized TAG_SEQ-GCTTGAGGGG" 177 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGJ13H21"
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/lab_host="E.coli"
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AZ698405
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Institute for Genomic Research
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SEQ4-65TO79 (1-15) x FR0048612 (1-597)
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                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 763)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, and Traco, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, and Traco, M.
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                          and Fraser.C.M.
Mouse BAC End Sequences from
Unpublished (1999)
Other_GSSs: RPCI-23-240110.TV
                                                                                                                                                                                                                                                                                                                                                                                AZ698405 763 bp DNA linear GSS 24-JAN-2001 RPCI-23-240L10.TJ RPCI-23 Mus musculus genomic clone RPCI-23-240L10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, M.S.
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1 (bases 1 to 597)
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                                                                                                                                                                                                                                             Mus musculus
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171 c 163 g 119 t
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/db_xref="taxon:31033"
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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: January 28, 2003, 13:16:53 Job time: 1271.67 secs
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                                                                               Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 240 row: L column: 10
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Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-240L10"
/clone_lib="RPCI-23"
/sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh

-MODEL-frame+_p2n.model -DEV-xlh

-Orcgn2_1/USBTO_Spool_MORINN82/runat_23012003_130141_7891/app_query.fasta_1.597

-DB-Issued_Patents_NA -OFMT-fastap -SUFFIX-olip2n.rn1 -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blts -STARF=1 -END=-1 -MATRIX-olip0 -TRANS-human40.cd1

-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN-8 -ALIGN=50 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000

-OSER-BORIN682_@CGN_1_1_25_@runat_23012003_130141_7891 -NCPU-6 -TCPU-3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WARIT -LONGLOG -DEV_TIMEOUT=120

-MARN_TIMEOUT=30 -THREADS=1 -XGAPOD=60 -XGAPEXT=60 -FGAPEXT=7

-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Perfect score:
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No matches found
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                                                                                 Score
                                                                                                                                                                                                                                                                                                                                          Issued_Patents_NA:*

1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/3

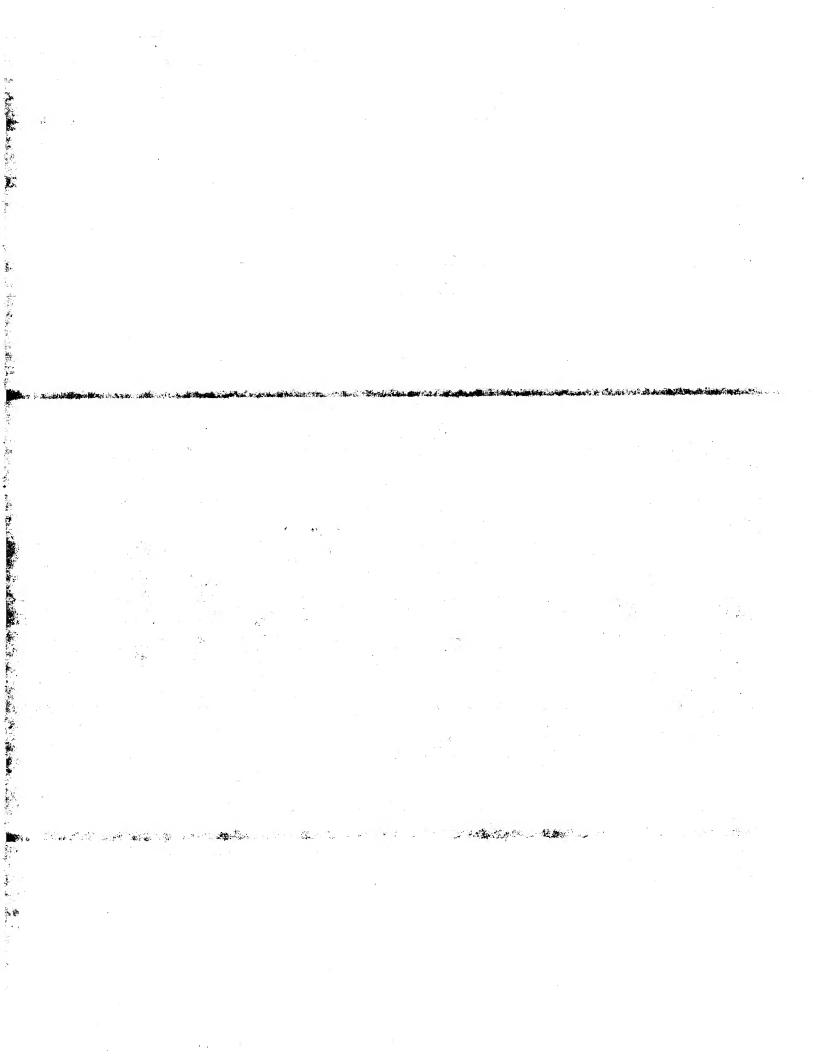
3: /cgn2_6/ptodata/3

4: /cgn2_6/ptodata/3

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6: /cgn2_6/ptodata/3
                                                                                 Match Length DB
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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Search completed: January 28, 2003, 13:19:48 Job time: 54 secs



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-OB=Published_Applications_NA -QFMT=fastap_SUFFIX=0.1ip2n .rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0-ligo
-TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=8
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NCGU=6 -LCGU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NCE_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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The invention structure of deleted from combined tand (A subunit ge having a subun a vector expression of the cultured. The vaccine. The toxin (mLT) A subunit struct Sequence 23	WPI; 2 Prepar Claim	07-AUG (DOKU- (HGET (FUJI-	Escheri JP20020 19-FEB- 07-AUG-	ABB07780; 17-JUN-2002 E coli muta LT; heat-la vaccine; mu	SULT 1 B07780 ABB077	113 113 114 115 116 117 117 118 118 118 118 119 118 119 119 119 119
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having a subunit ng each signal is gene and they are (SD sequence gene)-eparation of a protein we DNA is connected to and Brevibacillus transformant is on of an adjuvant for il mutant heat-labileing a protein with the				nt. adjuvant;		E coli heat-labile E. coli heat-labil E. coli heat-labil "Tys-63" E.coli he "Tyr-97" E.coli he "Tyr-97" E.coli he "Glu-107" E.coli h "Asp-104" E.coli h "Asp-104" E.coli h "Ser-104" E.coli h "Ser-104" E.coli h "Glu-114" E.coli h "Glu-114" E.coli h "Lys-114" E.coli h "Lys-114" E.coli h "Lys-114" E.coli he "Tyr-13" E.coli he "Tyr-15" E.coli he "Tyr-53" E.coli he "Tyr-53" E.coli he "Tyr-53" E.coli he

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                                                                                                            toxin submit A (LT-A). This protein is used in a method resulting in a mutant LT-A protein which has the wild type Ala residue at position 72 changed to an Arg residue resulting in a toxin which retains its immunogenicity but is detoxified. Detoxification is defined in the specification as a reduction in toxicity relative to wild-type toxin, such that any residual toxicity is sufficiently low to allow use as an effective immunogenic composition in humans without significant side effects. The protein can be combined with an acceptable carrier in immunogenic compositions, optionally comprising an adjuvant and/or a second immunogenic antigen. Such compositions can be administered to prevent/treat disease in a subject e.g. traveller's diarrhoea in humans. The protein or compositions are especially administered as vaccines useful to prevent or treat infections by enterotoxigenic strain of
                                                                                    Sequence
                                                                                                                                                                                                                                             This sequence represents a fragment of an Escherichia coli heat labile toxin subunit A (LT-A). This protein is used in a method resulting in a
                                                                                                                                                                                                                                                                              Disclosure; Page -; 67pp; English.
                                                                                                                                                                                                                                                                                               Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                                                                                                                                                                                                                                                                Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli heat labile toxin (LT) A subunit fragment, used for constructing a protein with the subunstructure of 1A5B.
Pig scours vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOKU-) DOKURITSU GYOSEI HOJIN (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-2000; 2000JP-0238740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-2000; 2000JP-0238740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB07778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB07778 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine.
                                                                                                                                                                                                                                                                          65 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                1 SLRSAHLAGOSILSG
                                      encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                            240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                (first entry)
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toxin; diarrhoea
                                      the pig
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                                                                                                                                                                                                                                                                                                                                                                             100
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                                      scours heat labile toxin
                                                                                                                                                                    258 AA
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                       Score 15; DE Pred. No. 6.2); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A subunit fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOGYO SEIBUTSU
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                                                                                                                                                                                                                                                                                                                                                       6.2e-08;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                      (LT) LTA gene
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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E.coli NCIB 11932

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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN50205 is the gene sequence of the natural LTA gene. The LTA gene the site directed mutant SDMI (see AAN50206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP50191 standard; Protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New toxoid as inactivated form of toxin obtd. from organism transformed by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP145486-A.
New toxoid as inactivated form of toxin for use in vaccines
                                                                                                                                                                                          12-DEC-1983;
                                                                                                                                                                                                                                 12-DEC-1984;
                                                                                                                                                                                                                                                                           19-JUN-1985
                                                                                                                                                                                                                                                                                                                    EP145486-A
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1991
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                                           1985-148358/25.
DB; AAN50206.
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                                                                                                                                                 ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
                                                                                                        Harford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coded by the pig scours directed mutant SDM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             11932.
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6.6e-08;
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Matches
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                                                                                                                                                                                                                             New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat-labile toxin; LT-A; adjuvant; anti-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96646 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN50205 is the gene sequence of the natural LTA gene. The LTA gene the site directed mutant SDM1 (see AAN50206) is inactive. The
                                                                                                                                                             Example
                                                                                                                                                                                                          elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                (BOYC-) BOYCE THOMPSON (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                       Mason HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1998;
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15; Conser
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                                                                                                                                                             1; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli heat labile toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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Pred. No. 6.6
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6e-08;
s 0;
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This synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A) is encoded by a plant-codon optimized cDNA. The cDNA sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accompdate the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of a NcoI restriction site around the wasteless of the creation of the creat

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RESULT 7
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Matches 15
  This is (LT-A).
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                                                                                                                                                                                                                                                                                                                                                                                                      (BOYC-)
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adjuvant; anti-bacterial;
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                                                                              Example 2; Page -; 103pp; English.
                                                                                                                                  New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                              N-PSDB;
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DB; AAA51147.
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mutant S63K Escherichia coli heat-labile toxin (LT) A subunit The wild-type serine was replaced with lysine at residue 63 of
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/note= "20"
20...259
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Pred. No.
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6.7e-08;
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                       WPI; 2000-442653/38.
N-PSDB; AAA51544.
                                                               Mason HS,
                                                                                                                                                                     22-DEC-1999;
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                                                                                                                                                                                                                         WO200037609-A2
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                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                     (BOYC-) BOYCE THOMPSON INST PLANT RES
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                                                                                                                                           98US-0113507
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                                                                                                                                                                                                                                                                            211
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                                                                                                                                                                                                                                                              /label= R192G
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Pred. No.
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New polynucleotides encoding LT-A or CT-A polypeptides for the

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RESULT 9
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The wild-type arginine was replaced with glycine at residue 192 of the mature protein, which was caused by a codon change of TCC to A6G in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals % \left( 1\right) =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant-optimized E.
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                                                                                                                                   Example 3; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96650
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22-DEC-1999;
                                                                                                                                                                                                                                                                                                    WO200037609-A2
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                                                                                                                                          29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLRSAHLAGQSILSG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLRSAHLAGQSILSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AA;
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99WO-US30747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- mature_protein 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= signal_peptide
20..259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- R192G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      "the wild type arginine is replaced by glycine at position 192 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "the wild type serine is replaced by lysine at position 63 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S63K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
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Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
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19-FEB-2002.

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This is Escherichia coli heat-labile toxin (LT) A subunit (LT-A) double curvant $63K+R192G. The wild-type serine was replaced with lysine at CC residue 63 and wild-type arginine was replaced with glycine at residue CC 192 of the mature protein. The coding sequence contains plant-preferred CC codons and eliminates sequence motifs associated with spurious mRNA CC processing. A single codon insertion (GTG encoding valine) was made to CC accomodate the creation of a NcoI restriction site around the initiator CC methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) cC polypeptide and where activity as compared to the CC vild-type LT-A or CT-A polypeptide and where at least one of the codons CC is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B CC subunit (CT-B). The polynucleotides are useful for the transformation of CC plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the CC prophylactic or therapeutic treatment against E. coli or V. cholerae. CC more than the produce does not appear in the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformation of plant cells, use elicit immune responses in animals
                                                                                                                                                                                                                                                 E coli mutant heat-labile toxin (mLT) 5B-SD-lA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mason HS, Arntzen CJ
                                                                                                                                                                                                                                                                               17-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                     ABB07785;
                                                                                                                                                                                                                                                                                                                                                     ABB07785 standard; Protein; 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOYC-) BOYCE THOMPSON INST PLANT RES.
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-1998;
                             JP2002051779-A
                                                                            Peptide
                                                                                                            Peptide
                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                              LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant; vaccine; mutant; mLT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLRSAHLAGQSILSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0113507
                                                                            /note= "LT 5B subunit" 104..370
                                                                                                                               Location/Qualifiers
                                                                /note= "LT lA subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.
                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT 11
ABB07784
ID ABB07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                              M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a gene encoding a protein having a subunit structure of IA5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene)-(SD sequence gene)-(A subunit gene). A method is provided for the preparation of a protein having a subunit structure of IA5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli mutant heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 9-10; 27pp; Japanese.
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                    (DOKU-) DOKURITSU GYOSEI HOJIN (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                    07-AUG-2000; 2000JP-0238740
                                                                                            07-AUG-2000;
                                                                                                                   19-FEB-2002
                                                                                                                                         JP2002051779-A.
                                                                                                                                                                         Peptide
                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                             vaccine
                                                                                                                                                                                                                                                                       Ξ;
                                                                                                                                                                                                                                                                                                                     17-JUN-2002
                                                                                                                                                                                                                                                                                                                                           ABB07784;
                                                                                                                                                                                                                                                                                                                                                                 ABB07784 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin (mLT)
                                                                                                                                                                                                                                                                                                                                                                                                                          198
                                                                                                                                                                                                                                                                                          coli heat-labile toxin (LT) 5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                     heat-labile toxin; cholera toxin; CT; recombinant; adjuvant;
2002-299402/34
                                                                                                                                                                                                                                                                                                                                                                                                                          SLRSAHLAGQSILSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                           2000JP-0238740
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000JP-0238740
                                                                                                                                                               104..37
/note=
                                                                                                                                                                                                  Location/Qualifiers 1..103
                                                                                                                                                                                    /note= "LT 5B subunit"
                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                            . 373
                                                                                                                                                                                                                                                                                                                                                                                                                          212
                                                                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                               "LT 1A subunit"
                                                                                                                                                                                                                                                                                                                                                                  373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB Pred. No. 9.1); Mismatches
                                             NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 le-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                             HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 12
AAU00507
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene) (SD sequence gene). (A subunit gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli heat-labile toxin
           N-PSDB; AAS01506
                       WPI; 2001-281524/29
                                             Park EJ,
                                                                                           15-SEP-1999;
                                                                                                                                                                  WO200119998-A1
                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                           Misc_feature
                                                                                                                                                                                                                                                                          Misc_feature
                                                                                                                                                                                                                                                                                                 Misc_feature
                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                               Escherichia coli strain K88ac
                                                                                                                                                                                                                                                                                                                                                                    detoxified and immunologicallendotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli heat-labile enterotoxin (LT) mutant LTdel110/112.
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU00507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU00507 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a gene encoding a protein having a subunit structure of 1A5B in which the DNA sequence encoding each signal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABL40639
                                                                  (MOGA-)
                                                                                                                   15-SEP-1999;
                                                                                                                                           22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                             Heat-labile enterotoxin; LT; LTS63Y; LTdell10/112; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 7-8; 27pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
15; Conserv
                                                                     MOGAM BIOTECHNOLOGY
                                             Kim JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                           99WO-KR00555
                                                                                                                   99WO-KR00555
                                                                                                                                                                                                                                                                                                                                                                                immunologically active protein; ADP-ribosylation; Gs;
                                                                                                                                                                                                  /note=
257
                                                                                                                                                                                                                           /note=
58..72
/note=
61
                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                     note=
                                           Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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                                                                                                                                                                                        "Encoded by TG"
                                                                                                                                                                                                                                      "Forms the NAD-binding
                                                                                                                                                                                                                                                            "Important residue for
                                                                                                                                                                                                                                                                                    "Important residue for enzymatic activity"
                                                                                                                                                                                                              "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0%;
                                                                     RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA
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                                             Yum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.;
                                            Chung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2e-08;
                                                                                                                                                                                                                                                             enzymatic activity'
                                                                                                                                                                                                                                       site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 13
AAU00506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type LT. The substitution of Ser to Tyr at position 63 in LTS63y blocks NAD-binding. Deletion of Glu residues at positions 110 and 112 in LTG61110/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that regulates cAMP levels. The resulting increase in cAMP is the cause of diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested. Groups of mice were immunised with LTS63Y or LTdell10/112. The control groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunised with LTS63Y or LTdell10/112 contained high and compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 42-44; 48pp; English
                                                                                                                                                                                                                                                             Heat-labile enterotoxin; LT; LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosyl
                                                                                                                                                                                                                                                                                             E. coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents Escherichia coli heat-labile enterotoxin (LT) mutant LTdell10/112. LTS63Y (AAU00506) and LTdell10/112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant
 WO200119998-A1
                                Misc-difference
                                                                         Misc_feature
                                                                                              Misc-difference
                                                                                                                    Misc_feature
                                                                                                                                                             Misc_feature
                                                                                                                                                                                   Misc_feature
                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                  29-AUG-2001
                                                                                                                                                                                                                                                                                                                                        AAU00506
                                                                                                                                                                                                                                                                                                                                                            AAU00506 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                              Escherichia coli strain K88ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLRSAHLAGQSILSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel detoxified and immunologically active proteins (IT ) derived by site-directed mutagenesis of the Al subunit of wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                            immunologically active protein;
                                                      /note=
112
                                                                         /note-
110
                                                                                              /note=
                                                                                                                    /note=
61
                                                                                                                                       /note=
58..72
                                                                                                                                                                                            Location/Qualifiers
                                          /note-
                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                             enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.
                                                                                                                                                                                                                                                                                                                                                                                                                 97
                    "Encoded by
                                         "Important residue
                                                                                   "Substitution
                                                                                                      "Important residue for enzymatic activity"
                                                                                                                            "Forms
                                                                                                                                                 "Important residue for enzymatic activity"
                                                                                                                                                                     "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15;
Pred. No.
                                                                                                                              the
                                                                                                                                                                                                                                                                                            (LT) mutant LTS63Y
                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                               residue
                                                                                                                            NAD-binding
                                                                                   of wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 9.4e-08; ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                        for enzymatic activity"
                                                              for enzymatic activity"
                                                                                   type
                                                                                                                             site"
                                                                                                                                                                                                                                                            ADP-ribosylation; Gs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 380;
                                                                                   Ser to
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 14
AAR44016
ID AAR44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are two novel detoxilied and immunologically active proteins (LT type LT. The substitution of ser to Tyr at position 63 in LTS63y blocks CNAD-binding. Deletion of Glu residues at positions 110 and 112 in CIT type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that CC unit type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that CC regulates cAMP levels. The resulting increase in cAMP is the cause of CC diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities CC of mutant heat-labile endotoxins LTS63y and LTdell10/112 were tested. CC groups of mice were immunised with LTS63y or LTdell10/112. The control CC groups received phosphate buffered saline (PBS) alone. The serum and CC mice immunised with LTS63y or LTdell10/112 contained that CC mice immunised with wild-type LT. The LT mutants are CC compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an arth-or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents Escherichia coli heat-labile enterotoxin (LT) mutant LTS63Y. LTS63Y and LTdell110/112 (AAU00507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2;
                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                         08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                           AAR44016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR44016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as ad-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2001
                                                                           Misc-difference
                                                                                                                                                                                                    ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                       "Lys-63" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 39-41; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 AA;
                                                                                                                                                                                                                           site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-KR00555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-KR00555
                                                                         Location/Qualifiers
                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for preventing and treating diarrhoea, and as adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chang J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
"corresponds to position 63 in cholera toxin A subunit; wild-type Ser is substituted by Lys to reduce toxicity"
                                                                                                                                                                                                    activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.4e-08;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                           toxicity;
                                                                                                                                                                                                                                                   detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 15
AAR44017
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J. Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).

    useful as vaccines against infection
enterotoxin producing Escherichia coli

                                                                                                                                                                                                                enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-227320/28.
N-PSDB; AAQ51317.
                                                                                                                                                                                                                                                                                 08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09313202-A
 31-DEC-1991;
                         30-DEC-1992;
                                                  08-JUL-1993
                                                                           W09313202-A
                                                                                                                                          Misc-difference
                                                                                                                                                                               Escherichia
                                                                                                                                                                                                     ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                          AAR44017;
                                                                                                                                                                                                                                                                                                                                 AAR44017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLRSAHLAGO 10
                                                                                                                                                                                                                                                                                                                                                                                             SLRSAHLAGQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                       E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA;
                                                                                                                                                                               coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                              (first entry)
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91IT-0MI3513
                         92WO-EP03016
                                                                                                                                                                                                                                                      heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCLAVO SPA
                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hol W,
                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
                                                                                                                                                                                                                                                      labile toxin subunit A.
                                                                                                                                                                                                       activity
                                                                                                 "corresponds to position 97 in cholera toxin A subunit; wild-type Val is substituted by Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pizza
                                                                                                                                                                                                                                                                                                                                 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 10; DB 14;
red. No. 0.0091;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rappuoli R;
                                                                                                                                                                                                                              detoxified LT-A;
                                                                                                                                                                                                                 toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 16
AAR44018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR4016-R44025). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequence and the description given in the text. (N.B. Amino sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxigenic bacteria;
protomer A; site-directed
ADP-ribosyltransferase act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                            WPI; 1993-227320/28
                                                                                                                                                                                                                                                                                                     30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9313202-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR44018 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-227320/28
N-PSDB; AAQ51318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domenighini M,
                                                                                            Domenighini M,
                                                                                                                                                                  (BIOC-)
                                                                                                                                                                                                                                      31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR44018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SLRSAHLAGQ 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                  BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                      91IT-0MI3513
                                                                                                                                                                                                                                                                                                     92WO-EP03016
                                                                                               Hol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hol
                                                                                                                                                                  SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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100.0%
                                                                                                                                                                  SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "corresponds to position 97 i
A subunit; wild-type Val is
Tyr to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
                                                                                               Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                            Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
0.0091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in cholera to
s substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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0;

N-PSDB; AAQ51319

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AAR44019
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutain is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin producing Escherichia coli
                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                  Ney Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
           Claim
                                                                                                                                                                                                                    08-JUL-1993
                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR44019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR44019 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                     Domenighini M,
                                                                                                                                                                      31-DEC-1991;
                                                                                                                                                                                           30-DEC-1992;
                                                                                                                                                                                                                                            W09313202-A
                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                  "Glu-107"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SLRSAHLAGQ 10
                                                                                              1993-227320/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numbering is based on the cholera toxin A subunit sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                   AAQ51320
                                                                                                                                             BIOCINE
          Fig 2
                                                                                                                                                                                                                                                                                                                                                                                                                  E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA;
                                                                                                                                                                                                                                                                                                                                            coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
           and
                                                                                                                     Ho1
                                                                                                                                                                    91IT-0MI3513
                                                                                                                                                                                           92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
                                                                                                                                             SCLAVO SPA.
                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
           Page
                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%
                                                                                                                                                                                                                                                                "corresponds to position 107 A subunit; wild-type His is Glu to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                   activity.
           46;
                                                                                                                     Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
          60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB
Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
                                                                                                                    Rappuoli R;
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0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                              detoxified LT-A;
toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                              substituted
                                                                                                                                                                                                                                                                                          in cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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RESULT 18
AAR44020
ID AAR444020
ID AAR444020
ID AAR44
XX AAR4
XX AAR44
XX PLys-
XX Esche
XX PT Misc-
FT Misc-
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al., J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; imm
protomer A; site-directed mutagenesis;
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                                                                                                                                                                                                               2 and Page 46; 60pp;
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                                                                      The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamotto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino
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                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                    Page 46; 60pp; English.
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A subunit; wild-type Tyr is
Asp to reduce toxicity"
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                                                   toxin A subunit sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in cholera toxin substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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В Qy

64

1 SLRSAHLAGQ SLRSAHLAGQ

10

Matches

10;

Conservative

0;

0;

Indels

0;

Gaps

0;

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RESULT 20
AAR44022
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                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J. Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutchin is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxigenic bacteria; protomer A; site-directed ADP-ribosyltransferase act
                                                                       Sequence
                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                   enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-227320/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOC-) BIOCINE SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR44022 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLRSAHLAGQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ51323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli heat
                                                                         236
                                                                                                                                                                                                                                                                                                                                                                                  detoxified mutant cholera toxin and heat labile toxin vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site-directed mutagenesis;
transferase activity.
                                                                                                                                                                                                                                                                                                                                                                 producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                         AΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91IT-0MI3513
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                  66.7%;
100.0%;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "corresponds to position 104 A subunit; wild-type Tyr is Ser to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
Score 10; DB; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogenic
sis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit
                  DB 14;
0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detoxified LT-A;
                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in cholera substituted
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RESULT 21
AAR44023
ID AAR44
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AAR44024
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                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutain is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 2 and Page 46; 60pp; English.
                                       AAR44024 standard; Protein; 236
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxigenic bacteria; vaccine; immu
protomer A; site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxin producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic detoxified mutant cholera toxin and heat labile toxin
useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOC-) BIOCINE SCLAVO SPA.
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                                                                                                                                               64
                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                1 SLRSAHLAGQ 10
                                                                                                                                             SLRSAHLAGQ 73
                                                                                                                                                                                                                                                                                                                                                        numbering
                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli
                                                                                                                                                                                                                                                                                                                  236 AA;
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                            is based
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heat labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                  66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "corresponds to position 106 A subunit; wild-type Pro is Ser to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                          on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza
                                                                                                                                                                                                                                                                                                                                                     the cholera toxin A subunit sequence)
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                    Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxin subunit A.
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                                       A
                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogenic
sis; reduced
                                                                                                                                                                                                                                                DB 14;
0.0091;
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detoxified LT-A;
toxicity;
                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                            Indels
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RESULT 23
AAR44025
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Best Local Similarity
Matches 10; Conser
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enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers Misc-difference 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                             AAR44025;
                                                                                                                    AAR44025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domenighini M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1993
                                       "Lys-114" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1992;
                                                                                                                                                                                      64
                                                                                                                                                                                                   1 SLRSAHLAGQ
                                                                                                                                                                                      SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1993-227320/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ51325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                 (first entry)
                                                                                                                                                                                                                                                                                            ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91IT-0MI3513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOl W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                    Protein;
                                                                                                                                                                                                                                                    66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "corresponds to position 114 in cholera toxin A subunit; wild-type Ser is substituted by Glu to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pizza
                                                                                                                                                                                                                                     Score 10; DB; Pred. No. 0.0
                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rappuoli R;
                                                                                                                                                                                                                                     DB 14; I
0.0091;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detoxified LT-A;
toxicity;
 toxicity;
             detoxified
                                                                                                                                                                                                                                                                Length 236;
                                                                                                                                                                                                                                        Indels
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ADP-ribosyltransferase

activity

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RESULT 24
AAR38728
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                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                                                                                                                                                                                                                                                  protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutch is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.coli heat labile toxin subunit A
                                                                                                                                                                                              AAR38728 standard;
08-JUL-1993
                        WO9313202-A
                                                                       protomer A; site-directed mutagenesis;
ADP-ribosyltransferase activity.
                                                                                               enterotoxigenic bacteria; vaccine;
                                                                                                                                               08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterotoxin producing Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ51326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1992;
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                                              Escherichia coli.
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                                                                                                                                                                                                                                                        1 SLRSAHLAGQ 10
||||||||||
64 SLRSAHLAGQ 73
                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                         236 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                              (first entry)
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                                                                                                                                                                                               Protein; 236 AA
                                                                                                                                                                                                                                                                                                                    66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "corresponds to position 114 A subunit; wild-type Ser is Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pizza
                                                                                                                                                                                                                                                                                                        0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                 immunogenic detoxifie
is; reduced toxicity;
                                                                                                                                                                                                                                                                                                      DB 14; I
0.0091;
thes 0;
                                                                                               detoxified LT-A;
                                                                                                                                                                                                                                                                                                                              Length 236,
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substituted
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RESULT 25
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the sequence of the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans. The sequence was published by Yanamoto et al, J.Biol. Chem., 259, 5037-5044. Mutations at selected positions within this sequence have been found to reduce toxicity (see AAR38730-R38732 and AAR44016-R44025). The invention relates to such immunogenic, detoxified proteins and their use in vaccines to protect against enterotoxigenic E.coli.
                                                                                                                                                                                                                                                     enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity.
N-PSDB; AAQ51314
          WPI; 1993-227320/28
                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                 "Asp-53" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
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                               Domenighini M,
                                                      (BIOC-)
                                                                          31-DEC-1991;
                                                                                                30-DEC-1992;
                                                                                                                      08-JUL-1993
                                                                                                                                             WO9313202-A.
                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                       SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
10; Conserv
                                                      BIOCINE SCLAVO SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                          91IT-0MI3513
                                                                                                 92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                       73
                                Hol W,
                                                                                                                                                                                                 Location/Qualifiers 52
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                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                               "corresponds to position 53 in cholera to
A subunit; wild-type Val is substituted
Asp to reduce toxicity"
                                Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                   236
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M
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                               Rappuoli
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0.0091;
                                70
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                                                                                                                                                                                                                                                                  toxicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 236;
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3;
            Claim
                                  enterotoxin
                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                 enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                   N-PSDB;
                                                                                                WPI; 1993-227320/28
                                                                                                                      Domenighini M,
                                                                                                                                                                                               30-DEC-1992;
                                                                                                                                                                                                                        08-JUL-1993
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                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                      ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                      "Glu-53" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1993
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          3; Fig
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                                                                                                                                                BIOCINE
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                                                                                                                                                                                                                                                                                                                                               coli
                                  producing
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                                                                                                                      Hol
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                                                                                                                                              SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
100.0%;
                                    Escherichia
                                                                                                                                                                                                                                                                     "corresponds to position 53 in cholera A subunit; wild-type Val is substitute Glu to reduce toxicity"
         46; 60pp; English
                                                                                                                       Pizza
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Pred. No.
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0.0091;
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                                                                                                                                                                                                                                                                                             toxin
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RESULT 27
AAR38732
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Best Local S
Matches 10
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       The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
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                                                                                                          Claim
                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                         WPI; 1993-227320/28
                                                                                                                                                                                                                                                                                                                      30-DEC-1992;
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                                                                                                                                                                                                                                                               (BIOC-)
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                                                                                                        3; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli.
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                                                                                                          2 and Page 46;
                                                                                                                                                                                                                                                                                            91IT-0MI3513
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.
                                                                                                                                                                                                                                      Pizza
                                                                                                        60pp;
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                                                                                                          English
                                                                                                                                                                                                                                   Rappuoli
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0.0091;
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toxicity;
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Best Local
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                                                                                                                                                                               This sequence corresponds to the amino acid sequence of the A subunit of the E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered parenterally in conjunction with at least one antigen in methods to immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell-mediated immune responses elicited by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification; parenteral adjuvant; antigen; antigen; immunisation; humoral response; cell-mediated immune response; virus; bacterium; parasite; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
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                      prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli heat labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW67772;
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                                                                                                                              the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1A-B; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1998;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9842375-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour; allergen; pathogen; AIDS; autoimmune disease; cancer;
systemic lupus erythematosus; Alzheimer's disease; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999
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DB; AAV81595.
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in the compositions and a pharmaceutically
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97US-0041227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment
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Pred. No.
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. 0.0091;
ches 0;
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RESULT 29
AAU14105
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                                                                              The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (ANU12559-ANU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrier. The antigen may be derived from viruses, bacteria, parasit, and fungi or may be tumour antigens, self-antigens and allergens. The compositions are therefore useful in the treatment and prevention of e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites), AIDS, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e.g. Systemic Lupus Erythematosus), Alzheimer's disease and cancers The adjuvant can also be used to prepare antibodies against selected antigen(s), useful e.g. for diagnostic purposes or for antigen
              including small molecule compounds, which may themselves exhibit antifusogenic, antivital or intracellular modulatory activity. The DP178-11ke-DP107-11ke peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The
                                                                                                                                                                                                                                                                                                                                      Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antivior intracellular modulatory activity, by detecting the formation of DP107/DP178 complex -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-retroviral; DP178-like; DP107-like; heat labile enterotoxin antifusogenic; antiviral; HIV transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide sequence from Escherichia coli heat labile enterotoxin A.
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                                                                                                                                                                                                                                                                                                     Disclosure; Fig 43; 259pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeffs P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
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100.0%
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawless MK,
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0.0092;
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                                                                                                                                                                                                                                                                                                                                                                            antiviral
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present sequence represents a peptide sequence from Escherichia

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Cc heat labile enterotoxin A.

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S0 Sequence 284 AA;

Guery Match Similarity 10.0%; Profit 10: DB 22; Length 254;

Guery Match Similarity 10: Profit 10: 0.0057; Indels 0: Gaps 0;

GY 1 SIRSAHIAGO 10

DB 2 SIRSAHIAGO 10

Search completed: January 28, 2003, 10:32:17

Job time: 127 secs
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A;Cross references: GB:R01995; NID:g148027; PIDN:AAA24685.1; PID:g148028
R;Spicer, E.K.; Noble, J.A.
J. Biol. Chem. 257, 5716-5721, 1982
A;Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subunit A;Reference number: A01817; MUID:82167425; PMID:6279611
A;Accession: A01817
A;Molecule type: DNA
A;Residues: 1-21, 'R', 23-36, 'FRS', 40-44, 46-92, 'Y', 94-99, 'LTIYI', 105-107, 111-118, 'IS', 121-A;Cross-references: EMBL:V00275; NID:g41339; PIDN:CAA23532.1; PID:g41340
                                                                                                                                                                                                                                                                                              heat-labile enterotoxin A precursor - Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Apr-1981 #sequence_revision 17-Oct-1997 #text_change 18-Jun-1999
C;Accession: I55231; A01817; A26946
R;Yamamoto, T.; Tamura, T.; Yokota, T.
J. Biol. Chem. 259, 5037-5044, 1984
A;Title: Primary structure of heat-labile enterotoxin produced by Escherichia coli pathd A;Reference number: I55231; MUID:84185610; PMID:8325417
A;Accession: I55231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-258 < RES>
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Maximum DB
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                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Score Match Length DB
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pir3:*
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A;Gene: eltA
C;Superfamily: heat-labile enterotoxin chain A
C;Keywords: enterotoxin
C;Keywords: enterotoxin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-258/Product: heat-labile enterotoxin chain A #status predicted
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J. Bacteriol. 169, 1352-1357, 1987
A;Title: Evolutionary origin of pathogenic determinants 1 A;Reference number: A26946; MUID:87137303; PMID:3546273 A;Accession: A26946
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA , Residues: 1-21, 'R', 23-206, 'N', 208-230, 'E', 232-255, 'D', 257-258 < YAM> A; Cross-references: EMBL:M15363 C; Comment: The heat-labile enterotoxin molecule contains one A chain and five or
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C;Genetics:
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[2]
                                                                                                           STRAIN-078:H11 / H10407;
MEDLING-84185610; PubMed-6325417;
Yamamoto T., Tamura T., Yokota T.;
"Primary Structure of heat-labile enterotoxin coli pathogenic for humans.";
J. Biol. Chem. 259:5037-5044(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                      P43530;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat-labile enterotoxin A chain precursor (LT-A,
               REVISION TO 207.
STRAIN-078:H11 / H10407;
MEDLINE-87137303; PubMed-3546273;
                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma
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ELAP_ECOLI STANDARD;
P06717; P01554;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36 Last annotation update)
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ACT_SITE
CONFLICT
             SEQUENCE FROM N.A.
STRAIN-Isolate PCG86, and Isolate P307;
MEDLINE-87137303; PubMed-3546273;
                                                                                    Bacteria; Proteobacteria; Escherichia.
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-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED INTE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
                                                                                                                 Escherichia coli
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EMBL; S60731; AAC60440.1;
HSSP; P06717; 1LTG.
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MEDLINE=93252225; PubMed=8486
Inoue T., Tsuji T., Koto M.,
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J. Bacteriol. 169:1352-1357(1987).
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SEQUENCE FACE. .... RESTRAIN-ISOLATE P307;
STRAIN-ISOLATE P307;
Dykes C.W., Halliday I.J., Hobden A.N., R
"A comparison of the nucleotide sequence
"A comparison of the nucleotide sequence
labile enterotoxin and cholera toxin.";
labile enterotoxin and cholera toxin.";
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MEDLINE=91238966; PubMed=2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Witholt B., Hol W.G.J.;
"Crystal structure of a cholera toxin-related heat-l from E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuji T., Inoue T., Miyama A., Okamoto K., Honda T., Miwata "A single amino acid substitution in the A subunit of Esche coli enterotoxin results in a loss of its toxic activity.", Biol. Chem. 265:22520-22525(1990).
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Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
"Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.";
Mol. Microbiol. 15:1165-1167(1995).
-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixma T.K., van Zanten B.A.M., Dau 
"Refined structure of Escherichia 
close relative of cholera toxin."; 
J. Mol. Biol. 230:890-918(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Isolate P307;
MEDLINE=82167425; Pu
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                                                                                                                      entities requires a or send an email to
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                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EDuropean Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
           M15361;
M15362;
M35581;
V00275;
W57244;
M61015;
A04913;
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J.D., Maas W.K.;
d (JUL-1991) to the
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license@isb-sib.ch)
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l Similarity 100
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01-AUG-1998 (TREMBLrel. 07, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation update)
Heat-labile enterotoxin A subunit.
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Vaccine 12:1083-1089(1994).

EMBL; AB011677; BAA25725.1; -.

EMSP; P06717; 1LTG.

InterPro; IPR001144; Enterotoxin_A.

InterPro; IPR00186; ER_target.

Pfam; PP01375; Enterotoxin_A; 1.

PRINTS; PR00771; ENTEROTOXINA,

PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

SEQUENCE 258 AA; 2931 MW; 2BB15D2774
                                                                                                                                                                                                                                                                                                                                        MEDLINE-95091056; PubMed-7998417;
Tamura S., Asanuma H., Tomita T., Komase K.,
Hattori N., Watanabe K., Suzuki Y., Nagamine
                                                                                                                                                                                                                                                                                                   "Escherichia coli heat-labile enterotoxin B subunits supplemented with a trace amount of the holotoxin as an adjuvant for nasal influenza
                                                                                                                                                                                                                                                                                                                            Kurata
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; Sequence 3, Application US/08823120
Patent No. 6149919
; GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic D
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TITLE OF INVENTION: Their Use for
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US-08-484-223B-114

US-08-919-597-114

US-08-475-668A-114

US-08-485-551A-114

US-08-485-524A-114

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Best Local Similarity
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Domenighini, Mario
APPLICANT: Domenighini, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Toolera Toxin and of the Toxin Lt, Their Preparation
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (510 (655-3542 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315
TELECOMMUNICATION INFORMATION:
                                             ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                            STREET: 4500
STREET: Emeryville
CITY: Emeryville
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 11-NOV-1994
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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CITY: Emeryville
STATE: California
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CLASSIFICATION:
                 FILING DATE:
                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COPUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/OOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPANE: (212) 790-9090
TELEFAN: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6:
                                                                                INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                               FILING DATE: 0: CLASSIFICATION:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/486,099 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315.001
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                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
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                                               LENGTH:
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                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                               New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Petteway, Stephen R.
Langlois, Alphonse J
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unknown
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Pred. No.
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В
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Best Local Similarity
"arches 10; Conserva
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US-08-360-107A-124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 124, Application US/08360107A Patent No. 6017536
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Matches 10; Conservative
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                                                                                                                                                                                                  TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Petteway, Stephen R.
APPLICANT: Langidois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBERANE FUSION-ASSOCIATED EVENTS, IN
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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 82
                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 20-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 A
CITY: New York
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                                                                                                                                                            STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                   1 SLRSAHLAGO 10
SLRSAHLAGO 91
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10036-2711
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                                                         Conservative
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Matthews, Thomas J.
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                                                                                                                                                 unknown
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100.0%; Pr
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100.0%; Pr
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                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                             7872-013
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Pred. No.
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                                                         Mismatches
                                                                     DB 3;
0.004;
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0.004;
                                                                                   Length 254;
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US-08-484-223B-114; Sequence 114, Application US/08484223B

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Best Local :
                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                             Sequence 114, Application US/08919597
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GENERAL INFORMATI
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SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
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                                APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Letteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TOTEEPY. (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                    CORRESPONDENCE ADDRESS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                 APPLICANT:
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STATE: New York
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ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                              82 SLRSAHLAGQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/484,223B
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1155 Avenue of the Americas
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Petteway, Stephen R.

Petteway, Stephen R.

Langlois, Alphonse J.

VENTION: COMPOSITIONS FOR INHIBITION OF

VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

VENTION: TRANSMISSION
                                                                                                                                                                                                               Bolognesi, Dani P.
Matthews, Thomas J.
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Botognesi, Thomas J.
                                                                                                                                                                                             Wild, Carl T.
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Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%; Score 10; DB 3; Length 254; 100.0%; Pred. No. 0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 114, Application US/08475668A
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
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MEDIUM TYPE: Floppy disk
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                     CITY: New York
STATE: New Yor
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STRANDEDNESS:
                                                                                                                                                                                  ZIP: 10036-2711
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                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
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Lambert, Dennis M.
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                                                     US/08/475,668A
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3. 0.004;
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US-08-485-551A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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                                                                                                                                                                                                                                                                                                                           NAME: COTUZZI, LAURA A.
REGIZANIA NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/485,551A
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MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
                            TOPOLOGY: ur
MOLECULE TYPE:
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TITLE OF INVENTION:
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                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                             LENGTH:
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                                                                                                                              amino acid
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1155 Avenue of the Americas
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Langlois, Alphonse J.
IVENTION: METHODS FOR INHIBITION OF MEMBRANE
IVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Lambert, Dennis M.
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                                                           unknown
                                                                                                                                                             amino acids
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100.0%; Pr
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Pred. No.
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0.004;
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US-08-485-264A-114
Sequence 114, Application US/08485264A; Patent No. 6228983; GENERAL INFORMATION:
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                                                              RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                    NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
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APPLICANT:
APPLICANT:
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                           82 SLRSAHLAGQ
                                                                                                                                                                       Local Similarity
nes 10; Conserv
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TOPOLOGY: ur
                                                                                                                                                                                                                                                                                  LENGTH: Zor
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                            254 amino acids
                                                                                                                                                                     66.7%; Score 10; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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100.0%;
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Pred. No.
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APPLICANT: Bolognesi, Dani P.

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RESULT 11
US-08-474-349A-114
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               APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Lembert, Dennis M.

APPLICANT: Lenglois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

TITLE OF INVENTION: VIRUS TRANSMISSION

TITLE OF INVENTION: VIRUS TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
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NAME: COTUZZI, Laura A.
REGISTRATION UMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: prote
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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New York
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Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
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0.004;
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; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-474-349A-114
Search completed: January 28, 2003, 10:38:03 Job time: 23 secs
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ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAUVA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
IFNORTH: 724 ATTOR SECIES
                                                                                                                                                               Matches
                                                                                                                                                                                  Query Match
Best Local Similarity
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
                                                                                  82 SLRSAHLAGQ 91
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                                                                                                                      1 SLRSAHLAGO 10
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100.0%; Pred. No.
tive 0; Mismatc
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RESULT 1
US-09-819-917-7
; Sequence 7, Application US/09819917
; Patent No. US2002004939A1
; GENERAL IMPORMATION:
GENERAL IMPORMATION:
APPLICANT: Fontana, Mariagrazia
APPLICANT: Giannelli, Valentina
APPLICANT: Rappuoli, Rina
TITLE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin
FILE REFERENCE: CHIR0312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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Maximum DB seq length: 2000000000
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Perfect score:
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CURRENT APPLICATION NUMBER: US/09/819,917
CURRENT FILING DATE: 2001-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                               15 100.0
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Gapop 60.0 , Gapext 60.0
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: //cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
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: //cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
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                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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; PRIOR APPLICATION NUMBER: 08/981/208
; PRIOR FILING DATE: 1997-12-22
; PRIOR PELING DATE: 1997-06-30
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENCTH: 240
; TYPE: PRT
; ORGANISM: E. coli
US-09-819-917-7

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 1 SLRSAHLAGOSILSG 15
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Db 65 SLRSAHLAGOSILSG 79

Search completed: January 28, 2003, 10:38:58
Job time: 13.333 secs
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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No matches found
                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                Query
Score Match Length DB
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Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA191.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA198.DAT:*
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Search completed: January 28, 2003, 10:32:17 Job time: 127 secs

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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                        APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           STREET: 4560 Hort
                                                          COUNTRY:
                                                                                       STATE:
                                             ZIP: 94608-2916
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Score Match Length DB

    Application US/08823120
    6149919

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                                                                                     California
                                                                                                                              E: Chiron Corporation 4560 Horton Street
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19.189 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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В
Search completed: January 28, 2003, 10:38:03 Job time : 23 secs
                                                                                                                                                                                                                                     US-08-823-120-1
                                                                                                                                                                                                                                                                                                         TELEPHONE: (510) 601-2708
TELEPAX: (510 (655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acids
GERENDERNIEGE. cid.
                                                                                                                                                                          Best
                                                                                                                                                          Matches
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/256
APPLICATION NUMBER: US 08/256
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0315
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                            6 VPNNKEFK 13
|||||||
186 VPNNKEFK 193
                                                                                                                                                      Match 53.3%; Someone Similarity 100.0%; Nes 8; Conservative 0;
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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linear
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b; Pred. No. 0.1
0; Mismatches
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lo. 0.11;
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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US-09-819-917-5

Sequence 5, Application US/09819917

Sequence 5, Application US/09819917

Patent No. US20020044939A1

GENERAL INFORMATION:

APPLICANT: Pizza, Mariagrazia

APPLICANT: Fontana, Maria Rita

APPLICANT: Roptoni, With Maria Rita

APPLICANT: Rappuoli, Rina

APPLICANT: Rappuoli, Rina

TITLE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin

FILE REFERENCE: CHIR0312

CURRENT APPLICATION NUMBER: US/09/819,917

CURRENT FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                       Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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SEQ ID NO 5
LENGTH: 241
TYPE: PRT
ORGANISM: E. COLI
US-09-819-917-5
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Search completed: January 28, 2003, 10:38:58
Job time: 13.3333 secs
                                                                                                           Matches
                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/981,208
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: 9513371.6
                                                                                                                                                                                                                                             PRIOR FILING DATE: 1995-06-30 NUMBER OF SEQ ID NOS: 8
                                                    6 VPNNKEFK 13
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186 VPNNKEFK 193
                                                                                                          Local Similarity
les 8; Conserv
                                                                                                           Conservative
                                                                                                                      53.3%;
                                                                                                          0;
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Pred. No. 0.039;
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A; Molecule type: DNA
A; Residues: 1-259 <PIC>
A; Residues: 1-259 <PIC>
A; Cross-references: GB:M17894; NID:g146671; PIDN:AAA24093.1; PID:g146672
A; Note: the authors translated the codon TAT for residue 225 as Thr
C; Superfamily: heat-labile enterotoxin chain A
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-259/Product: heat-labile enterotoxin IIa chain A #status predicted <LTA>
                                                                                                                                                                                                                                                            C;Accession: A29831
R;Pickett, C.L.; Weinstein, D.L.; Holmes, R.K.
J. Bacteriol. 169, 5180-5187, 1987
A;Title: Genetics of type IIa heat-labile enterotoxin of Escherichia coli: operon fusion A;Reference number: A91849; MUID:88032841; PMID:2822667
A;Accession: A29831
                                                                                                                                                                                                                                                                                                                                                                                                                    heat-labile enterotoxin IIa chain A precursor - Escherichia coli
N;Alternate names: LT-IIa
C;Species: Escherichia coli
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
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No.
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Maximum DB seq length: 2000000000
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Perfect score:
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Query Match 60.0%; Score 9; DB 2; Ler Best Local Similarity 100.0%; Pred. No. 0.0056; Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Score Match Length DB
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15
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Copyright (c) 1993 - 2003 Compugen Ltd.
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9

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Qy 6 VPNNKEFKG 14
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Search completed: January 28, 2003, 10:33:46 Job time : 25.6667 secs

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P13810;
                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-88032841; PubMed=2822667;

MIEDILINE-88032841; PubMed=2822667;

Pickett C.L., Weinstein D.L., Holmes R.K.;

Pickett G.L., Weinstein D.L., Holmes R.K.;

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Benetics of type IIa heat-labile enterotoxin of Production Studies.";

J. Bacteriol. 169:5180-5187(1987).

"IB ACHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

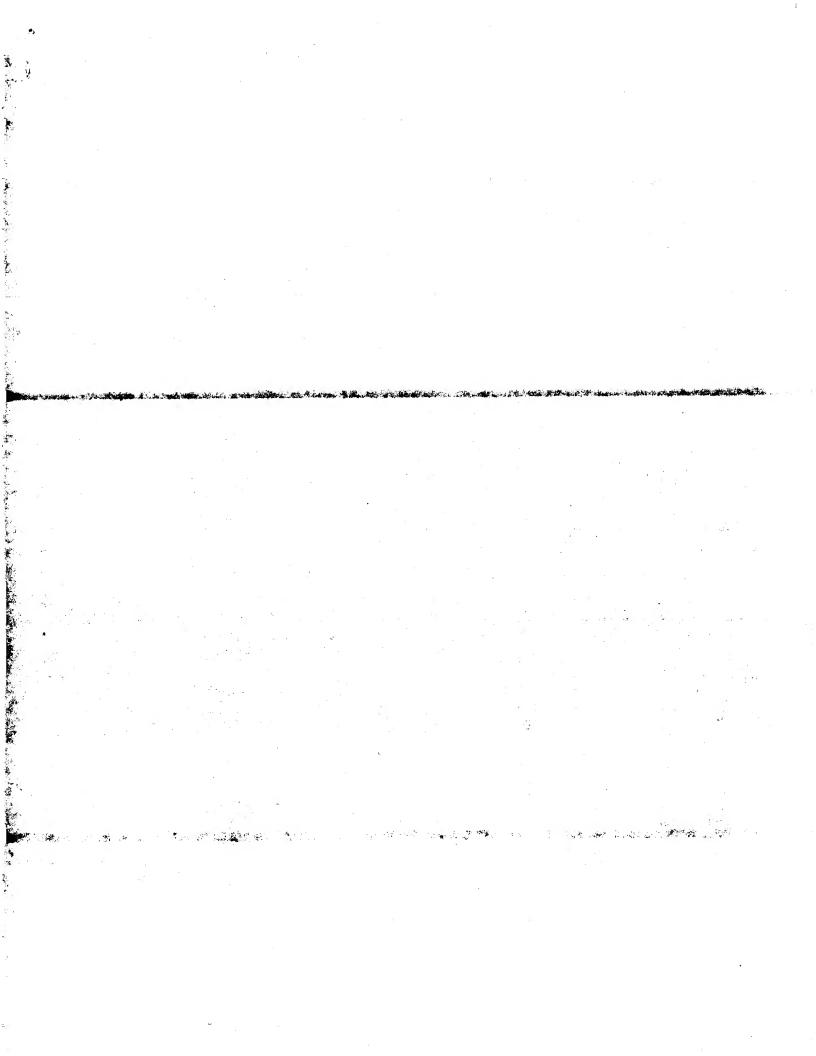
"THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

"THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."

"THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."
                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECOLI
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                     NCBI_TaxID-562;
                                                                                                                                                                                                                                                                                                                             Escherichia
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15
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                                                                                                                                                                                                                                                                                                                                                                                   enterotoxin IIA, A chain precursor (LT-IIA).
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(without alignments)
53.327 Million cell updates/sec
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                                        Query Match 60.0
Best Local Similarity 100
Matches 9; Conservative
                                                                                 DISULFID
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                InterPro; IPR001144; Enterotoxin_A.
Pfam; PF01375; Enterotoxin_A; 1.
PRINTS; PR00771; ENTEROTOXINA.
                                                                                                                                                                                 PIR; A29831; A29831.
HSSP; P43528; 1TII.
                                                                                                                           SIGNAL
                                                                                                                                      Enterotoxin; Signal.
                                                                                                                                                                                                      EMBL; M17894; AAA24093.1;
                                                                                                                   CHAIN
204 VPNNKEFKG
            6 VPNNKEFKG 14
                                                                               19
203
128
259
                                                                                   AA;
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259
215
B
128
B; 29242 MW;
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                                                                                 HEAT-LABILE ENTEROTOXIN IIA, A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
; 996F311A32CABEAA CRC64;
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b. 0.0021;
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                                          Indels
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Search completed: January 28, 2003, 10:25:42 Job time: 11.6667 secs



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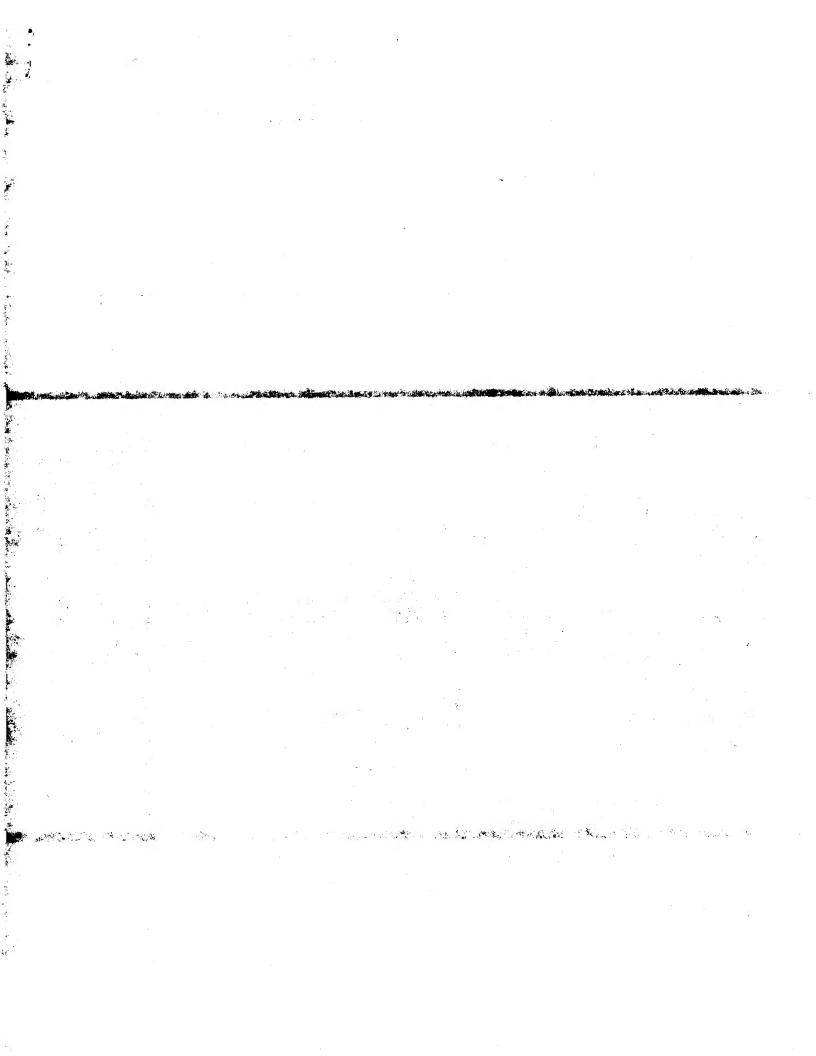
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GenCore version 5.1.3 Compugen Ltd.
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Result
No.
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                 SPTREMBL_21:*

1: sp_bacteria:
2: sp_bacteria:
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb:
6: sp_mamma1:*
7: sp_mhc:*
8: sp_organe11:
9: sp_phage:*
10: sp_plant:*
11: sp_virus:*
12: sp_virus:*
13: sp_vertebr
13: sp_vertebr
14: sp_unclass
15: sp_bacteri
16: sp_bacteri
17: sp_archeap
 Query
Match Length DB
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15
1 STFEQVPNNKEFKGV 15
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                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
sp_fung1:*
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Search completed: January 28, 2003, 10:36:40 Job time : 53.333 secs

No matches found



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Search completed: January 28, 2003, 10:32:17 Job time: 127 secs
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                                                                                                                                                 No matches found
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Score Match Length DB
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

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6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

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12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

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14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

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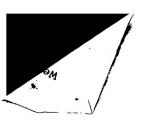
25: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

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29: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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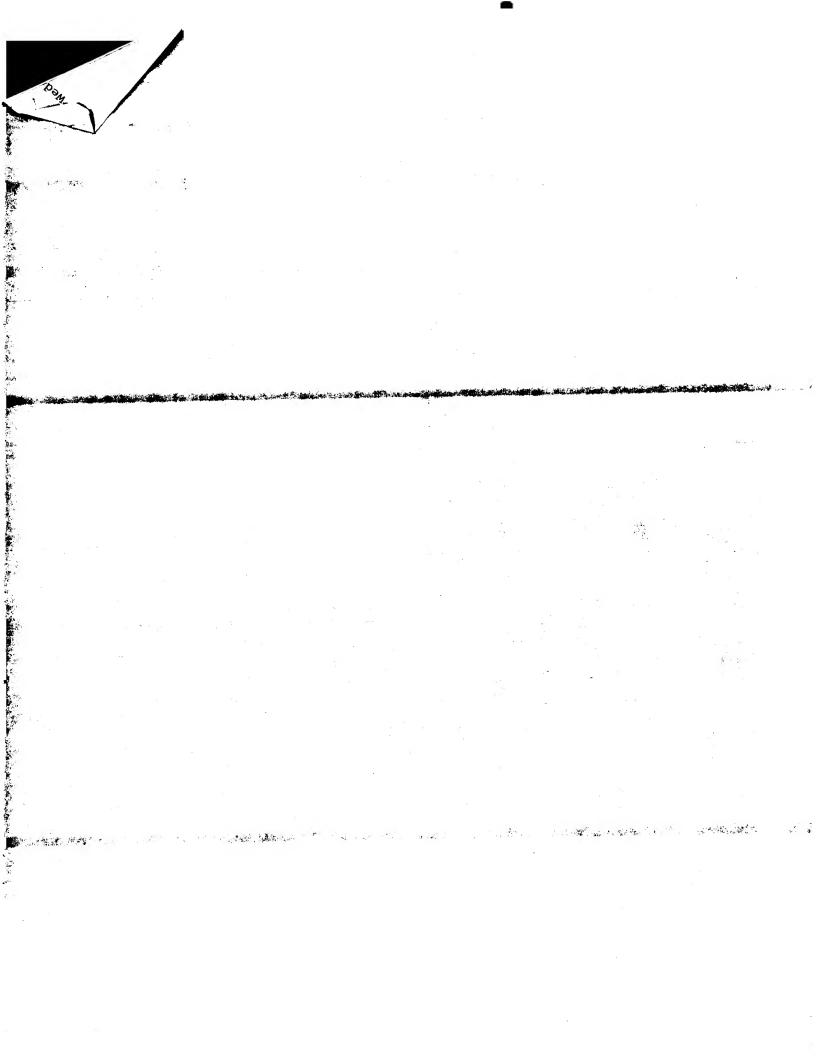


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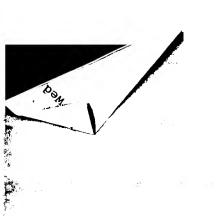
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Total number of hits satisfying chosen parameters:
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Perfect score:
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No. Score Match Length DB ID
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Search completed: January 28, 2003, 10:33:46 Job time: 24.6667 secs
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                                                                             No matches found
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                                                                                                                                                                                                                                                                                                                         PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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15
1 REFNSLPNNKASSDT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.3 Compugen Ltd.
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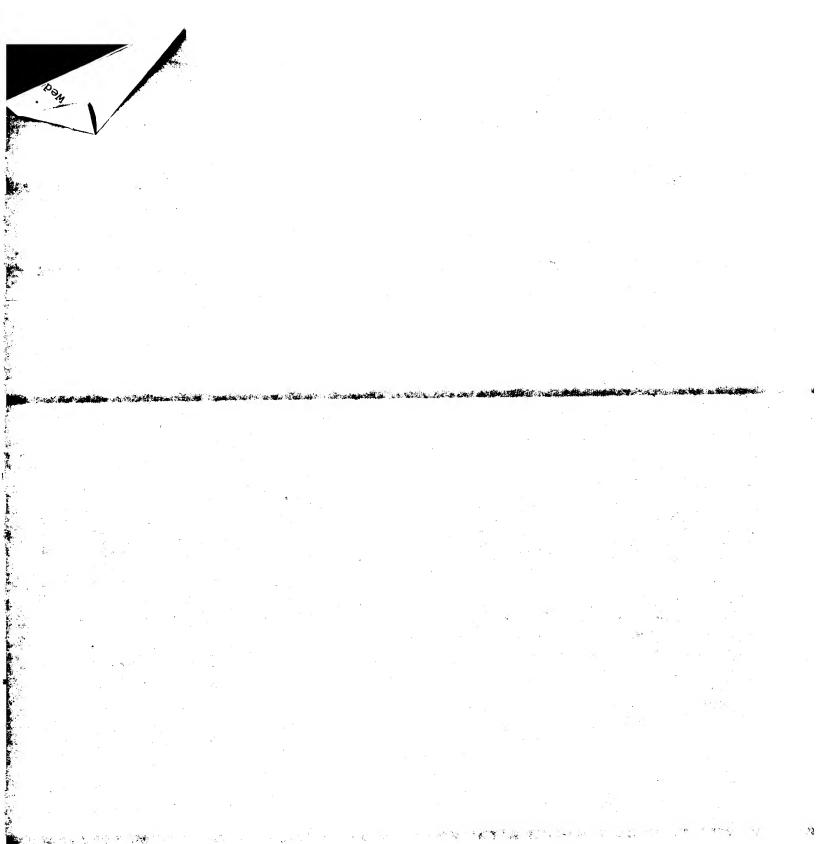
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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                  E2BA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO.
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                                                                                                                                                                                                                                                                                                                  P43528;
01-NOV-1995
01-NOV-1995
15-JUN-2002
"Crystal structure of a new heat-labile enterotoxin, LT-IIb."; Structure 4:665-678(1996).
                                                                                                         STRAIN-Isolate 41;
MEDLINE-89359131; PubMed=2670900;
MIDLINE-89359131; PubMed=2670900;
Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;
"Cloning, nucleotide sequence, and hybridization studies of the type IIb heat-labile enterotoxin gene of Escherichia coli.";
J. Bacteriol. 171:4945-4952(1989).
                                                            X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS). MEDLINE-96399713; PubMed-8805549;
                             van den Akker F.,
Hol W.G.J.;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 Heat-labile enterotoxin
                                                                                                                                                                                                                                      NCBI_TaxID=562;
                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                      Escherichia coli
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length: 2000000000
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Match Length DB
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Gapop 60.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
enterotoxin IIB, A chain precursor (LT-IIB).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                              Sarfaty S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003, 10:24:52 ;
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                                            Twiddy E.M., Connell T.D., Holmes R.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                  263
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(without alignments)
53.327 Million cell updates/sec
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                   CHAIN
                                                                                                                                                                               SIGNAL
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                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                        SEQUENCE
                                                                                                                                                                                               Enterotoxin; Signal;
                                                                                                                                                                                                            PRINTS; PR00771; ENTEROTOXINA
                                                                                                                                                                                                                               Pfam;
206 LPNNKASSDT 215
                            6 LPNNKASSDT 15
                                                                                                                                                                                                                             PF01375; Enterotoxin_A; 1.
                                                                                                                      263 AA;
                                                                                                                                      205
130
                                                          Conservative
                                                                                                                                    20
263
217
130
                                                    66.7%; 5--
100.0%; Pr/
0;
                                                                                                                      29485 MW;
                                                                                                                                                                                                 3D-structure.
                                                                       Score 10;
Pred. No.
                                                                                                                                                                   HEAT-LABILE ENTEROTOXIN IIB, A CHAIN.
                                                                                                                      A56E8A069427CFB9 CRC64;
                                                            Mismatches
                                                                       DB 1; L, 0.00064;
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                                                                                        Length 263;
                                                            Indels
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                                                          Gaps
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Search completed: January 28, 2003, 10:25:42 Job time: 11.6667 secs



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Result
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Search completed: January 28, 2003, 10:36:40 Job time: 53.3333 secs
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Maximum DB seq length: 200000000
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                                                               No matches found
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Score Match Length DB
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1 REFNSLPNNKASSDT 15
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1: sp_archea:
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sp_bacteria:*
sp_fungi:*
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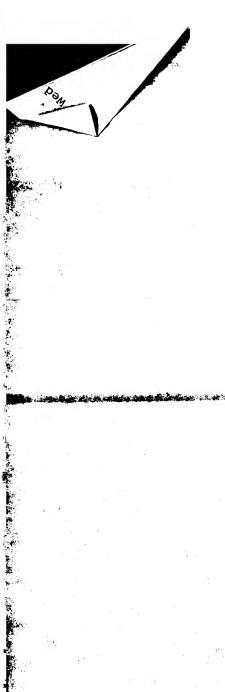
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Gapop 60.0 , Gapext 60.0
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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19.189 Million cell updates/sec
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Search completed: January 28, 2003, 10:38:03 Job time: 23 secs



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No matches found
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1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

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13: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

16: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

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Search completed: January 28, 2003, 10:38:58 Job time: 13.3333 secs

